

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2005, 11:18:45; Search time 11952 Seconds
(without alignments)
11528.839 Million cell updates/sec

Title: US-10-734-801-18

Perfect score: 2771
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 2771 | 100.0 | 5860 | 6 | AR478127 Sequence |
| 3 | 2674 | 96.5 | 2674 | 6 | AR478129 Sequence |
| 4 | 2327 | 84.0 | 2327 | 6 | AR478130 Sequence |
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| 6 | 1773.2 | 64.0 | 5917 | 12 | AB037684 Cloning v |
| 7 | 1766 | 63.7 | 6192 | 12 | AF416989 Synthetic |
| 8 | 1763.2 | 63.6 | 5064 | 6 | AX339209 Sequence |
| 9 | 1763.2 | 63.6 | 5064 | 6 | U47297 Cloning vec |
| 10 | 1763.2 | 63.6 | 5256 | 6 | AX339208 Sequence |
| 11 | 1763.2 | 63.6 | 5256 | 12 | U47296 Cloning vec |
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| 14 | 1758.2 | 63.1 | 7718 | 6 | AX528380 Sequence |
| 15 | 1747.2 | 63.1 | 7312 | 6 | AX528381 Sequence |
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| c | 27 | 1657.6 | 59.8 | 10820 | 12 | AY603761 Cloning v |
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ALIGNMENTS

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| RESULT 1 | AR478128 | Sequence 18 from patent US 6699657. | DNA | linear | PAT 14-MAY-2004 |
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| ACCESSION | AR478128 | | | | |
| VERSION | AR478128.1 | GI:47236755 | | | |
| KEYWORDS | Unknown. | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unknown. | | | | |
| REFERENCE | Unclassified. | | | | |
| AUTHORS | King, R.W., Jeffries, M.W. and Pasquinel, C. | | | | |
| TITLE | In vitro system for replication of RNA-dependent RNA polymerase | | | | |
| JOURNAL | (RDRP) viruses | | | | |
| FEATURES | Patent: US 6699657-A 18 02-MAR-2004; | | | | |
| source | Location/Qualifiers | | | | |
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| | /organism="unknown" | | | | |
| | /mol_type="genomic DNA" | | | | |
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| QY | 121 | CTCCCGACAGGACAGAAATGCAAGCATCTCAATTAGTCAGCAACATAGTCC 180 | | | |
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ACCESSION AR478127
VERSION AR478127.1 GI:47236754
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5860)
AUTHORS King, R.W., Jeffries, M.W. and Pasquinelli, C.
TITLE In Vitro System for Replication of RNA-dependent RNA polymerase
(RDRP) viruses
JOURNAL Patent: US 6699657-A 17 02-MAR-2004;
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Qy 2701 TGGCGCGGCTGCGCAACATTCGAGGAGACCGTCTCTGATATGCGAAATGGAACCC 2760
Db 2701 TGGCGCGGCTGCGCAACATTCGAGGAGACCGTCTCTGATATGCGAAATGGAACCC 2760
Qy 2761 ACAATCTCTC 2771
Db 2761 ACAATCTCTC 2771

RESULT 3
AR478129
LOCUS AR478129 2674 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 19 from patent US 6699657.
ACCESSION AR478129
VERSION AR478129.1 GI:47236756
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2674)
AUTHORS King,R.W., Jeffries,M.W. and Pasquinel1,C.
TITLE In vitro system for replication of RNA-dependent RNA polymerase
(JRDR) viruses
JOURNAL Patent: US 6699657-A 19 02-MAR-2004;
FEATURES
Location/Qualifiers
source 1..2674
/mol_type="genomic DNA"

ORIGIN
Query Match 96.5%; Score 2674; DB 6; Length 2674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATTCGCTGTGAATGCTGTCAGTTAGGCTGGAAGTCCCGAGGCTCCCGACAGG 60
Db 1 GATTCGCTGTGAATGCTGTCAGTTAGGCTGGAAGTCCCGAGGCTCCCGACAGG 60
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Qy 121 CTCGCCAGAGGAGGAATGCAAAAGCATGATCTCAATTAGTCAGCAACGATGTC 180
Db 121 CTCGCCAGAGGAGGAATGCAAAAGCATGATCTCAATTAGTCAGCAACGATGTC 180
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Db 181 GCCCCTAATCCGCCCATCCGCCCTTAATCTCCGCCAATTCGCCCATTCGCCGCA 240
Qy 241 TGGTACTAATTTTTTATTTATTTATGACAGGCGGAGCGGCTCGGCTCTGAGTAT 300
Db 241 TGGTACTAATTTTTTATTTATTTATTTATGACAGGCGGAGCGGCTCTGAGTAT 300
Qy 301 CCAAGATGATGAGAGGCTTTTGTGAGGCTTGAAGCTTTTGCAAAAGCTTATCATGATC 360
Db 301 CCAAGATGATGAGAGGCTTTTGTGAGGCTTGAAGCTTTTGCAAAAGCTTATCATGATC 360
Qy 361 TGAAGAGAGGAGATTCAGCACTCTCTGACATCAATGCGGCTCAGCGACTTTTCAAGCT 420
Db 361 TGAAGAGAGGAGATTCAGCACTCTCTGACATCAATGCGGCTCAGCGACTTTTCAAGCT 420

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|----|------|----------------------|--------------------------------|----------------------------------|------|
| OY | 421 | AGCCGTGACTAGGCGCTT | AGATGAGACCCACATT | TAAGAGAGAGAAAGAAAGAAAA | 480 |
| Db | 421 | AGCCGTGACTAGGCGCTT | AGATGAGACCCACATT | TAAGAGAGAGAAAGAAAGAAAA | 480 |
| OY | 481 | AGAGGAAAGAA | AAAAAAAAAAAAAAAAAAAA | AGAAAAAGAAAAAGAAAAAGAAAA | 540 |
| Db | 481 | AGAGGAAAGAA | AAAAAAAAAAAAAAAAAAAA | AGAAAAAGAAAAAGAAAAAGAAAA | 540 |
| OY | 541 | AAAAAAAAAAAAAAAAAAAA | AAAAAAAAAAAAAAAAAAAA | CAGAAATGGCTT | 600 |
| Db | 541 | AAAAAAAAAAAAAAAAAAAA | AAAAAAAAAAAAAAAAAAAA | CAGAAATGGCTT | 600 |
| OY | 601 | GGCCGGAGGT | TACCCCACTTT | TAAGGGGACTTTTCCGCCCTTCTTGGCCTTT | 660 |
| Db | 601 | GGCCGGAGGT | TACCCCACTTT | TAAGGGGACTTTTCCGCCCTTCTTGGCCTTT | 660 |
| OY | 661 | AGGATCTCT | GTATTTTCTTGCGTGA | ATTTTCCGGTAAGACCTTTCGGTACTTGCTCC | 720 |
| Db | 661 | AGGATCTCT | GTATTTTCTTGCGTGA | ATTTTCCGGTAAGACCTTTCGGTACTTGCTCC | 720 |
| OY | 721 | ACAAACAACA | CTTCCTCGCGCACTTTT | CGCGGTGTACTTGACTGGCGAGTATCC | 780 |
| Db | 721 | ACAAACAACA | CTTCCTCGCGCACTTTT | CGCGGTGTACTTGACTGGCGAGTATCC | 780 |
| OY | 781 | AGGATCTCT | TTTCCGTCACTGCTTCCGTGCTCA | AAACAACAACGGCGGGAGAT | 840 |
| Db | 781 | AGGATCTCT | TTTCCGTCACTGCTTCCGTGCTCA | AAACAACAACGGCGGGAGAT | 840 |
| OY | 841 | TCACCGGCGTCA | TGTCGGGAAGACTGCGACA | CTTGCCTGAGATGTGGGCTGTGG | 900 |
| Db | 841 | TCACCGGCGTCA | TGTCGGGAAGACTGCGACA | CTTGCCTGAGATGTGGGCTGTGG | 900 |
| OY | 901 | AGCAAGATG | AGATTTCCAATTACGGGGAGCACCTGA | TACCTTTGATCTTAATCAAGAC | 960 |
| Db | 901 | AGCAAGATG | AGATTTCCAATTACGGGGAGCACCTGA | TACCTTTGATCTTAATCAAGAC | 960 |
| OY | 961 | TTTCAGCGGTCA | ACGATGAGAGATGTGCTTGCCTCCAGTAA | AGCTATGTCTCCAGAA | 1021 |
| Db | 961 | TTTCAGCGGTCA | ACGATGAGAGATGTGCTTGCCTCCAGTAA | AGCTATGTCTCCAGAA | 1021 |
| OY | 1021 | TGTAGCCAT | CCATCTCTTGTCAATCAAGCGGTGTGCTT | CCGGATTTGTTTACATPACCG | 1081 |
| Db | 1021 | TGTAGCCAT | CCATCTCTTGTCAATCAAGCGGTGTGCTT | CCGGATTTGTTTACATPACCG | 1081 |
| OY | 1081 | GACATATCATATG | AGACTCTCACACACAGTGGCCTT | TGATTAACGCCCGACGCTTTC | 1141 |
| Db | 1081 | GACATATCATATG | AGACTCTCACACACAGTGGCCTT | TGATTAACGCCCGACGCTTTC | 1141 |
| OY | 1141 | CCGGATATCA | GATTCACAACTTGGCTTCAAAAAAT | TGAAACAATTACCGACCGCGCC | 1201 |
| Db | 1141 | CCGGATATCA | GATTCACAACTTGGCTTCAAAAAAT | TGAAACAATTACCGACCGCGCC | 1201 |
| OY | 1201 | GTTTATATAT | CCCCCTCGGGTGTAAATCA | AAATAGCTGATGTACTCACTGAGCCCATAT | 1261 |
| Db | 1201 | GTTTATATAT | CCCCCTCGGGTGTAAATCA | AAATAGCTGATGTACTCACTGAGCCCATAT | 1261 |
| OY | 1261 | CCTTGCCTGAT | ATCCTGGCAGATGGAACCTT | TGGCAACCGCTTCCCGCATCTTCTTAGAG | 1321 |
| Db | 1261 | CCTTGCCTGAT | ATCCTGGCAGATGGAACCTT | TGGCAACCGCTTCCCGCATCTTCTTAGAG | 1321 |
| OY | 1321 | AGGGAGGGCC | ACCAAGAACTTTCGTGTAAATTA | GAATTAATCGATTTTGTCAATCAGA | 1381 |
| Db | 1321 | AGGGAGGGCC | ACCAAGAACTTTCGTGTAAATTA | GAATTAATCGATTTTGTCAATCAGA | 1381 |
| OY | 1381 | GTGCTTTTGG | CCAGAGAGATAGGTTTGGCACACAGCGGCA | CTTTGAATCTTTGTA | 1441 |
| Db | 1381 | GTGCTTTTGG | CCAGAGAGATAGGTTTGGCACACAGCGGCA | CTTTGAATCTTTGTA | 1441 |
| OY | 1441 | TCCTGAAGGCT | CTCTCAGAAACGCTTCTTCAAT | CTATACATTAAGCACTGAAAT | 1501 |
| Db | 1441 | TCCTGAAGGCT | CTCTCAGAAACGCTTCTTCAAT | CTATACATTAAGCACTGAAAT | 1501 |

| | | | |
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| QY | 1501 | COACATATCAAAATATCCGATGTGTAAACATTCGAAAACCGTGATGGAATGGAACAACA | 1560 |
| Db | 1501 | CCACATATCAAAATATCCGATGTGTAAACATTCGAAAACCGTGATGGAATGGAACAACA | 1560 |
| QY | 1561 | CTTAAATATCGAGATATCCGGAATGATTTGATTTGGCAAAATATAGGATCTCTGGCATGGAG | 1620 |
| Db | 1561 | CTTAAATATCGAGATATCCGGAATGATTTGATTTGGCAAAATATAGGATCTCTGGCATGGAG | 1620 |
| QY | 1621 | AATCTCAGCAGCAGGAGTTCTATGAGGCGAGACGACCTTTTAGCGAGACCAATAGATATCA | 1680 |
| Db | 1621 | AATCTCAGCAGCAGGAGTTCTATGAGGCGAGACGACCTTTTAGCGAGACCAATAGATATCA | 1680 |
| QY | 1661 | GAGAGATTCAATGATCATGTGCAATTGTGTTCCTATGAGAGACTGTGGCACAAAATCG | 1740 |
| Db | 1661 | GAGAGATTCAATGATCATGTGCAATTGTGTTCCTATGAGAGACTGTGGCACAAAATCG | 1740 |
| QY | 1741 | TATTCATTAAACCGGGAGGTATGATGAGATCTGACGAACTGTATCATGCACTGAAATCC | 1800 |
| Db | 1741 | TATTCATTAAACCGGGAGGTATGATGAGATCTGACGAACTGTATCATGCACTGAAATCC | 1800 |
| QY | 1801 | TGTTATCCGTTTAAATCATATATATATTTTGGATGATTTGGAGCTTTTTTTTC | 1860 |
| Db | 1801 | TGTTATCCGTTTAAATCATATATATATTTTGGATGATTTGGAGCTTTTTTTTC | 1860 |
| QY | 1861 | ACGTTCAAAATTTTGTGCAACCCCTTTTGGAAAAGAACACACGAGTATGAGTGGCAAAATG | 1920 |
| Db | 1861 | ACGTTCAAAATTTTGTGCAACCCCTTTTGGAAAAGAACACACGAGTATGAGTGGCAAAATG | 1920 |
| QY | 1921 | CCCATATCTGTGACGAATTCAGCTTCATTAATAATGTCTCCGGGGGGGCAATGCAACT | 1980 |
| Db | 1921 | CCCATATCTGTGACGAATTCAGCTTCATTAATAATGTCTCCGGGGGGGCAATGCAACT | 1980 |
| QY | 1981 | CCGATAAATTAACGGCGCCCAACACGGGCTAATAAGATTGGAAGAGATTTCATCTCATACG | 2040 |
| Db | 1981 | CCGATAAATTAACGGCGCCCAACACGGGCTAATAAGATTGGAAGAGATTTCATCTCATACG | 2040 |
| QY | 2041 | ACGATTTCTGTATTTGTATTCAGCCCATATGCTTTCAATGCTTCTGCCAACCGAACGGAC | 2100 |
| Db | 2041 | ACGATTTCTGTATTTGTATTCAGCCCATATGCTTTCAATGCTTCTGCCAACCGAACGGAC | 2100 |
| QY | 2101 | ATTTCGAAGTACTCAGCGTAAATGATATGTCCACTTCGATATGTGCATCTGTAAAGCAATT | 2160 |
| Db | 2101 | ATTTCGAAGTACTCAGCGTAAATGATATGTCCACTTCGATATGTGCATCTGTAAAGCAATT | 2160 |
| QY | 2161 | GTTCCAGGAACACAGGGCGTATCTCTTACACTTAATGACATGTCCTCCACGGGTTTCCA | 2220 |
| Db | 2161 | GTTCCAGGAACACAGGGCGTATCTCTTACACTTAATGACATGTCCTCTCCACGGGTTTCCA | 2220 |
| QY | 2221 | TCTTTCAGCGGATATGAAATGAGCGCGGCGCTTCTTATATGTTTGTGCGCTTCTTCACATGGGA | 2280 |
| Db | 2221 | TCTTTCAGCGGATATGAAATGAGCGCGGCGCTTCTTATATGTTTGTGCGCGCTTCTTCACATGGGA | 2280 |
| QY | 2281 | CGTCGGTTGTGTTTACGTTTGTGTTTTCTTTAGAGTTTAGGATTCGTCTCATGTATGAC | 2340 |
| Db | 2281 | CGTCGGTTGTGTTTACGTTTGTGTTTTCTTTAGAGTTTAGGATTCGTCTCATGTATGAC | 2340 |
| QY | 2341 | GGTCTAGAGACCTCCCGGGGCACTCCGCAACACCTATCAGGGAGTATGCAACAAGGCTT | 2400 |
| Db | 2341 | GGTCTAGAGACCTCCCGGGGCACTCCGCAACACCTATCAGGGAGTATGCAACAAGGCTT | 2400 |
| QY | 2401 | TCGCGACCCCAACATCTACTCGCTAGCAGTCTTTCGCGGGGCAACGGCCAAATCTCCAGGCAT | 2460 |
| Db | 2401 | TCGCGACCCCAACATCTACTCGCTAGCAGTCTTTCGCGGGGCAACGGCCAAATCTCCAGGCAT | 2460 |
| QY | 2461 | TGAGCGGGGTTATCCAGAAAGAACCCGGGTGTCTTGGAATTCGCGGTATCTCAACCGGT | 2520 |
| Db | 2461 | TGAGCGGGGTTATCCAGAAAGAACCCGGGTGTCTTGGAATTCGCGGTATCTCAACCGGT | 2520 |
| QY | 2521 | TCGCGAGACCATATGAGCTCTCCGGGAGGGGGGGTCTTGAGGCTGACACACTCATTA | 2580 |
| Db | 2521 | TCGCGAGACCATATGAGCTCTCCGGGAGGGGGGGTCTTGAGGCTGACACACTCATTA | 2580 |
| QY | 2581 | CTAACCGCATGCTAGACGCTTTCTGCGTGAAGACATGATTTCTTCACAGGGGAGTGAATT | 2640 |

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Db      2581 CTTAACGCCATGGCTAGACGCTTTCTGCTGAAGACATGTTCTTCAAGGGAGTGATT 2640
Qy      2641 CATGTGAGTGTGCCCCCATCAGGGGGCTGGC 2674
Db      2641 CATGTGAGTGTGCCCCCATCAGGGGGCTGGC 2674

RESULT 4
AR478130
LOCUS   AR478130 2327 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 20 from patent US 669657.
ACCESSION AR478130
VERSION  AR478130.1 GI:47236757
KEYWORDS
SOURCE  Unknown.
ORGANISM Unknown.
REFERENCE 1. (bases 1 to 2327)
AUTHORS King, R.W., Jeffries, M.W. and Paquinelli, C.
TITLE In vitro system for replication of RNA-dependent RNA polymerase
(JDRP) viruses
JOURNAL Patent: US 669657-A 20 02-MAR-2004;
FEATURES Location/Qualifiers
source 1. 2327
/mol_type="genomic DNA"

ORIGIN
Query Match 84.0%; Score 2327; DB 6; Length 2327;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      348 AGCTTACATATCTGACAGAGGCGCATATCAGCACTCTGTGAGTCATGCGGCTCACGG 407
Db      1 AGCTTACATATCTGACAGAGGCGCATATCAGCACTCTGTGAGTCATGCGGCTCACGG 60
Qy      408 ACCTTTACAGCTAGCCGCTAGCTAGGCTTAAGTGGAGCCACCTTAAAGAAAGAA 467
Db      61 ACCTTTACAGCTAGCCGCTAGCTAGGCTTAAGTGGAGCCACCTTAAAGAAAGAA 120
Qy      468 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 527
Db      121 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 180
Qy      528 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 587
Db      181 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 240
Qy      588 AAATGGCTTAAGAGGCGGAGTGTATACCCCAACCTTTAAAGCGGCACTTTTCCGCCCTT 647
Db      241 AAATGGCTTAAGAGGCGGAGTGTATACCCCAACCTTTAAAGCGGCACTTTTCCGCCCTT 300
Qy      648 CTTGGCCTTATAGAGATCTCTGATTTTCTTTCGTCGAGTTTTCGGGTAAAGACCTTT 707
Db      301 CTTGGCCTTATAGAGATCTCTGATTTTCTTTCGTCGAGTTTTCGGGTAAAGACCTTT 360
Qy      708 CGGTACTTGTCTCAAAACAACCTCTCGCGCAACTTTTTCGGGTGTATGTA 767
Db      361 CGGTACTTGTCTCAAAACAACCTCTCGCGCAACTTTTTCGGGTGTATGTA 420
Qy      768 GGGAGGTATTCACGATCTCTTTTCCGTCATGCTTTCCGTCGCGTCCGAAACAAC 827
Db      421 GGGAGGTATTCACGATCTCTTTTCCGTCATGCTTTTCCGTCGCGTCCGAAACAAC 480
Qy      828 GGGCGCGGAGATTCACGCGGCTCATGTCGGGAAAGACTGCAACCTGCTGAAAGAT 887
Db      481 GGGCGCGGAGATTCACGCGGCTCATGTCGGGAAAGACTGCAACCTGCTGAAAGAT 540
Qy      888 GTTGGGTGTGGAAGAAATGATTCATTCAGCGGAGCAACCTGATAGCCTTTGTA 947
Db      541 GTTGGGTGTGGAAGAAATGATTCATTCAGCGGAGCAACCTGATAGCCTTTGTA 600
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Qy      948 CTTAATCAGAGACTTTCAGCGGCTCAACGATGAAGAGTGTGCTCTTCCGCCAGTAAAGC 1007
Db      601 CTTAATCAGAGACTTTCAGCGGCTCAACGATGAAGAGTGTGCTCTTCCGCCAGTAAAGC 660
Qy      1008 TATGCTCCGAAATGATGACCATTCATCTGTGAATCAAGGCGTGTGCTCCGAAATT 1067
Db      661 TATGCTCCGAAATGATGACCATTCATCTGTGAATCAAGGCGTGTGCTCCGAAATT 720
Qy      1068 GTTTAATTAACCGGACATTAATCATAGAACTCTCAACACAGTTGCGCTTTGATTAAC 1127
Db      721 GTTTAATTAACCGGACATTAATCATAGAACTCTCAACACAGTTGCGCTTTGATTAAC 780
Qy      1128 GCCACGGTTTTCCGGTATCCAGATCCACACTTGGCTTCAAAAAATGGAACAACCTTT 1187
Db      781 GCCACGGTTTTCCGGTATCCAGATCCACACTTGGCTTCAAAAAATGGAACAACCTTT 840
Qy      1188 ACCGACCGCGCCGGTTTATCATCCCCCTCGGGTGTATCAGAAATAGCTGATAGTCTC 1247
Db      841 ACCGACCGCGCGGGTTTATCATCCCCCTCGGGTGTATCAGAAATAGCTGATAGTCTC 900
Qy      1248 AGTGAAGCCATATCTTTGCTGATACCTGCGAGATGGAACCTTTGGCAACCGCTTCCC 1307
Db      901 AGTGAAGCCATATCTTTGCTGATACCTGCGAGATGGAACCTTTGGCAACCGCTTCCC 960
Qy      1308 GACTTCCTTAAGAGGGGAGCGCCACAGAAAGCAATTTGCTGTAAATGATTAATCGTA 1367
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Qy      1368 TTTGTCAATCAGAGTCTTTTGGCGAAGAAAGAAATAGGGTTGGCAGCAGCGCACT 1427
Db      1021 TTTGTCAATCAGAGTCTTTTGGCGAAGAAAGAAATAGGGTTGGCAGCAGCGCACT 1080
Qy      1428 TTGAATCTGTAAATCTCTGAAGGCTCTTCAAGAAACAGCTCTTTTCAATCTAATTA 1487
Db      1081 TTGAATCTGTAAATCTCTGAAGGCTCTTCAAGAAACAGCTCTTTTCAATCTAATTA 1140
Qy      1488 GACGACTCGAAATCCACATATCAAAATATCGAGTATGAATTCGAAATCCGGAATG 1547
Db      1141 GACGACTCGAAATCCACATATCAAAATATCGAGTATGAATTCGAAATCCGGAATG 1200
Qy      1548 GATGGAACAACCTTAAATCGCAGATATCCGGAATGATTTGATTCGCAAAATAGATC 1607
Db      1201 GATGGAACAACCTTAAATCGCAGATATCCGGAATGATTTGATTCGCAAAATAGATC 1260
Qy      1608 TCTGGCATGCGAATCTCAACGAGCGAGTTCTATAGGACAGAGCAACCTTTAGCGAG 1667
Db      1261 TCTGGCATGCGAATCTCAACGAGCGAGTTCTATAGGACAGAGCAACCTTTAGCGAG 1320
Qy      1668 ACCAGTATGATCCAGAGAGTTCATGATCAGTGAATTTGCTTCCCTATCCGAAGGATC 1727
Db      1321 ACCAGTATGATCCAGAGAGTTCATGATCAGTGAATTTGCTTCCCTATCCGAAGGATC 1380
Qy      1728 TGCGACAATAATCGTATTCATTAATAACCGGAGGTAGATGATGACCAACGCTATCAT 1787
Db      1381 TGCGACAATAATCGTATTCATTAATAACCGGAGGTAGATGATGACCAACGCTATCAT 1440
Qy      1788 CGACTGAATTCCTGTGTAATCCGTTTGAATTCATGATTAATTTTGGATGATGG 1847
Db      1441 CGACTGAATTCCTGTGTAATCCGTTTGAATTCATGATTAATTTTGGATGATGG 1500
Qy      1848 GAGCTTTTGTGACGTTCAAAATTTTGGCAACCCCTTTGGAAAGCAACACCGGCT 1907
Db      1501 GAGCTTTTGTGACGTTCAAAATTTTGGCAACCCCTTTGGAAAGCAACACCGGCT 1560
Qy      1908 AGGCTGCGAAATGCCCATCTGTTGAGCAATTCAGTTCAATTAATGTCGTCGCGG 1967
Db      1561 AGGCTGCGAAATGCCCATCTGTTGAGCAATTCAGTTCAATTAATGTCGTCGCGG 1620
Qy      1968 CCGAATGCAACTCCGATTAATTAACGCGCCAAACCGGCATTAAGAAATGGAAGAGTT 2027
Db      1621 CCGAATGCAACTCCGATTAATTAACGCGCCAAACCGGCATTAAGAAATGGAAGAGTT 1680
Qy      2028 TTCACCTGCAATAGACGATCTGTGATTTGTATTCAGCCCATATCGTTTATAGCTTCTGC 2087
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Db      1681 TTCACTGCATACGAGGATTCTGTGATTTGTATTCAGCCCATATCGTTTCATAGCTTTCG 1740
Qy      2088 CAACCGAAGCGACATTTTGAAGTACTCAGCGTAAGTATGTCACCTCGATATGTGCATC 2147
Db      1741 CAACCGAAGCGACATTTTGAAGTACTCAGCGTAAGTATGTCACCTCGATATGTGCATC 1800
Qy      2148 TGTAAAGCAATTTTCCAGGAACGAGGCGGTATCTCTTCATAGGCTTATGAGTTGCTC 2207
Db      1801 TGTAAAGCAATTTTCCAGGAACGAGGCGGTATCTCTTCATAGGCTTATGAGTTGCTC 1860
Qy      2208 TCCAGCGGTTCCATCTTCCAGCGGATAGATGAGCGCGGCTTTCTTTATGTTTTGGC 2267
Db      1861 TCCAGCGGTTCCATCTTCCAGCGGATAGATGAGCGCGGCTTTCTTTATGTTTTGGC 1920
Qy      2268 GTCTTCATGGAAGCGTGGTGTGTATTCAGTTGTTTTCTTTGAGTTAGATTGCT 2327
Db      1921 GTCTTCATGGAAGCGTGGTGTGTATTCAGTTGTTTTCTTTGAGTTAGATTGCT 1980
Qy      2328 GGTCAATGATGCAAGGCTTACGAGACCTCCGCGGCACTCCGCAAGCACTTATCAGGCACT 2387
Db      1981 GGTCAATGATGCAAGGCTTACGAGACCTCCGCGGCACTCCGCAAGCACTTATCAGGCACT 2040
Qy      2388 ACCAAGGCGCTTTGCGGCAAGCACTACTGCGTACGAGTCTTGCGGGGCAAGCCCA 2447
Db      2041 ACCAAGGCGCTTTGCGGCAAGCACTACTGCGTACGAGTCTTGCGGGGCAAGCCCA 2100
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Db      2161 TGTACTTACCGGTTCCGCAAGCACTATGCTCTCCCGGAGGGGGGCTCTCGAGGCTG 2220
Qy      2568 CACGACATCATACTTAACGCGCATGCTAGACGCTTTCTGCGGAAGACAGTATGCTCTCA 2627
Db      2221 CACGACATCATACTTAACGCGCATGCTAGACGCTTTCTGCGGAAGACAGTATGCTCTCA 2280
Qy      2628 CAGGGAGGATGATTCATGCTGAGTGTGCGCCCATCAGGGGCGCTGCG 2674
Db      2281 CAGGGAGGATGATTCATGCTGAGTGTGCGCCCATCAGGGGCGCTGCG 2327

RESULT 5
AB119282/
LOCUS      AB119282                9658 bp    RNA       linear   VRL 27-MAR-2004
DEFINITION Hepatitis C virus gene for Fusion protein, Feo, complete cds.
ACCESSION  AB119282
VERSION     AB119282.1 GI:37991671
KEYWORDS
SOURCE      Hepatitis C virus
ORGANISM    Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1
AUTHORS     Yokota, T., Sakamoto, N., Enomoto, N., Tanabe, Y., Miyagishi, M.,
            Maezawa, S., Yi, L., Kurosaki, M., Taira, K., Watanabe, M. and
            Mizusawa, H.
            Inhibition of intracellular hepatitis C virus replication by
            synthetic and vector-derived small interfering RNAs
            EMBO Rep. 4 (6), 602-608 (2003)
TITLE
JOURNAL     MEDLINE
PUBMED      22625416
REFERENCE   2
AUTHORS     Tanabe, Y., Sakamoto, N., Enomoto, N., Kurosaki, M., Ueda, E.,
            Maezawa, S., Yamashiro, T., Nakagawa, M., Chen, C.H., Kanazawa, N.,
            Kakimura, S. and Watanabe, M.
            Synergistic inhibition of intracellular Hepatitis C virus
            replication by combination of Ribavirin and Interferon- alpha
            J. Infect. Dis. 189 (7), 1129-1139 (2004)
TITLE
JOURNAL     PUBMED
PUBMED      15031779
REFERENCE   3
AUTHORS
            (bases 1 to 9658)

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AUTHORS    Tanabe, Y. and Sakamoto, N.
TITLE      Direct Submission
JOURNAL    Submitted (03-SEP-2003) Yoko Tanabe, Tokyo Medical and Dental
            University, Department of Gastroenterology and Hepatology; 1-5-45
            Yushima, Bunkyo-ku, Tokyo 113-8519, Japan
            (E-mail: ytanabe.gast@md.ac.jp, Tel: 81-3-5803-5877,
            Fax: 81-3-5803-0268)
FEATURES   location/Qualifiers
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            VLVNVRFEELFLRSIDYKIOSALVPTLSPFAKSLIDKYDLSNLAELASGAPL
            SKVEGAVALAKFPHLPGLRQGYGLTETTSAILITEGDDKPGAVGVVFPFAKVVLD
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            TEKELVDIVASQVTTAKKLRGVGVFVDEVPKGLTGDKDARKILRLIAKKGAKIAR
            RAMLEQDGLHAGSPAAWVERLFGVDMQOTTGCSDAVFAQRPLVFKTDLISGA
            LNELODEARLMSLATTGVCAPAVLDVVTENGRMMLLGEVPGDLSHLAPAKVS
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ORIGIN
Query Match      71.9%; Score 1992.2; DB 14; Length 9658;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2022; Conservative 0; Mismatches 13; Indels 12; Gaps 1;
Qy      628 ACGGCACTCTTCCGCCCTTCTTGCGCTTATAGAGATCTCTGATTTTCTTCCGCTG 687
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 SOURCE
 ORGANISM
 other sequences; artificial sequences.
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 1 (bases 1 to 5917)
 AUTORS Chen,A.B., Kao,A.Y.-F. and Brown,C.M.
 TITLE A short open reading frame within the encapsidation signal affects the translation of the polymerase gene from hepatitis Bvirus
 JOURNAL
 REFERENCE
 2 (bases 1 to 5917)
 AUTORS Chen,A.B., Kao,A.Y.-F. and Brown,C.M.
 TITLE Direct Submision
 JOURNAL Submitted (27-JAN-2000) Chris M. Brown, University of Otago, Department of Biochemistry, P.O.Box 56, Dunedin, Otago 9001, New Zealand (E-mail:chris.brown@stonebow.otago.ac.nz, Tel:+64-3-479-7875, Fax:+64-3-479-7866)
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| QY | 1620 | GAATTCACGCAAGCAGTCTTATATGAGAGAGAGCGCACACTTTATGAGCAGACAGTAGATATCC | 1679 |
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| SOURCE | synthetic construct | | |
| ORGANISM | synthetic construct | | |
| REFERENCE | other sequences: artificial sequences. | | |
| AUTHORS | 1 (bases 1 to 6192) | | |
| TITLE | Holen,T., Amarzguinolui,M., Wiger,M.T., Babaie,E. and Prydz,H. | | |
| JOURNAL | Positional effects of short interfering RNAs targeting the human | | |
| MEDLINE | coagulation trigger Tissue Factor | | |
| PUBMED | Nucleic Acids Res. 30 (8), 1757-1766 (2002) | | |
| REFERENCE | 21935767 | | |
| AUTHORS | 11937629 | | |
| TITLE | 2 (bases 1 to 6192) | | |
| JOURNAL | Holen,T., Amarzguinolui,M. and Prydz,H. | | |
| FEATURES | Direct Submission | | |
| SOURCE | Submitted (07-SEP-2001) The Biotechnology Centre of Oslo, | | |
| LOCATION/Qualifiers | University of Oslo, Gaustadalleen 21, Oslo 0373, Norway | | |
| 1..6192 | | | |

| | Query Match | Similarity | Score | DB | Length |
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ACCESSION AX339209
VERSION AX339209.1 GI:18135470
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.

REFERENCE 1
AUTHORS Yang, A.L. and Festing, M.
TITLE Methods and materials to determine the p53 status of a sample by
JOURNAL determining the binding of p53 to a vector
Patent: WO 019602-A 3 20-DEC-2001;
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ORIGIN

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Matches 2002; Conservative 0; Mismatches 168; Indels 108; Gaps 3;

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QY 1621 AATTCACGAGCAATTTCTATGAGGACAGAGCACTTTAGCGAGACCATGATGATCCA 1680
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QY 1861 ACGTCAAAATTTTGTGCAACCCCTTTTGTGAAAGCAACCAAGGATGAGCTGCGAAATG 1920
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ORIGIN

/home="KV primers sequencing primer binding site"

| Query Match | 63.6% | Score 1763.2 | DB 12 | Length 5064 |
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| Best Local Similarity | 87.9% | Pred. No. 0 | | |
| Matches 2002 | Conservative 0 | Mismatches 168 | Indels 108 | Gaps 3 |
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| DB | 2255 | GGATCCGCTGTGAAATGTGTCTCAGTTAGGGGTGTGAAAGTCCCGAGGCTCCCGACAGG | 2156 | |
| QY | 61 | CAGAAAGTATGCAAAAGCATCTCAATTGTATGCAACACGAGGTGGAAAGTCCCGAG | 120 | |
| DB | 2195 | CAGAAAGTATGCAAAAGCATCTCAATTGTATGCAACACGAGGTGGAAAGTCCCGAG | 2136 | |
| QY | 121 | CTCCCGACGACGACGAAGTATGCAAAAGCATCTCAATTAGTCAGCAACCATAGTCC | 180 | |
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| QY | 181 | GCCCCTAATCCCGCCATCCCGCCCTTAATCTCGGCCAGTTCGSCCATTTCTCGGCCCA | 240 | |
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| QY | 241 | TGGCTGACTAATTTTTTTTATTTATGAGAGGCGGAGCGGCTCTCGGCTCTGAGCTATT | 300 | |
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| QY | 301 | CCAGAAAGTATGAGAGGCTTTTGTGAGGCGCTTAGGCTTTTGCAAAAAGCTTACATGATC | 360 | |
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| QY | 361 | TGCAGAGAGGCCAATATCAGCACTCTGCGAGTCATCGGCTCAGGACCTTTACAGCT | 420 | |
| DB | 1967 | -----CTTTAAAAAACTCTCCACACCTCCCTGAACCTGAACCTTAATAATGAA | 1919 | |
| QY | 421 | AGCCGTGACTAGGCTAAGATGAGCAACATTAAAGAGAGAGAAAGAAAGAAAAA | 480 | |
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| QY | 481 | AGAGAGAGAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA | 540 | |
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| QY | 541 | AA | 600 | |

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Db      1223  |CCGGTATCCAGATCCACACCTTCCGTTCAAAAAATGAAACAATTTCAGACCGCGCC 1164
Qy      1201  |GGTTTATCATCCCGCTCGGGGTATGATGATAGCTAGTGAAGCCCATAT 1260
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Qy      1441  |TCTGAAAGGCTCTCAGAAAACAGCTCTTCTCAATCTATATCAATTAAGACGACTGAAAT 1500
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Qy      1801  |TGGTAAATCCGTTTAAATTCATGATTAATTTTGGATGATGATGGAAGCTTTTTCG 1860
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Qy      1861  |ACGTTCAAAATTTTTCGCAACCCCTTTTGGAAACGACCAACCGTAGCTCGAAATG 1920
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Qy      1921  |CCCATACGTGTGAGCAATTCAGTTCAATTAATGTCGTGCGGGCGCAACTGCAACT 1980
Db      443  |CCCATACGTGTGAGCAATTCAGTTCAATTAATGTCGTGCGGGCGCAACTGCAACT 384
Qy      1981  |CCGATAAATTAACGCGCCCAACACCGGCATTAAGAAATTTGATCTGCACTAGAC 2040
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Qy      2041  |ACGATCTGTGATTTTATTCACGCCATATCGTTTCAATAGCTTCTGCAACCGAC 2100
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Qy      2101  |ATTTCGAAGATCAACGATGATGATGTCACCTCGATATGTCATCTGTAAAGCAATT 2160
Db      263  |ATTTCGAAGATCAACGATGATGATGTCACCTCGATATGTCATCTGTAAAGCAATT 204
Qy      2161  |GTTCCAGAAACGAGGCGATATCTTTCATAGCCTTAATGCAAGTTGCTCCAGCGTTCCA 2220
Db      203  |GTTCCAGAAACGAGGCGATATCTTTCATAGCCTTAATGCAAGTTGCTCCAGCGTTCCA 144
Qy      2221  |TCTTCCAGCGGATGAAATGCGCGCGCTTTCTTATATGTTTGGCGTCTTCATGG 2278
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VERSION     AX339208.1 GI:18135469
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REFERENCE   1
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| | | | |
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| Oy | 61 | CAGAAATATGCAAAAGCATGTCACTTCAATTTAGTCAGCAACACAGGTGTGAAAGTCCCAAG | 120 |
| Db | 2387 | CAGAAATATGCAAAAGCATGTCACTTCAATTTAGTCAGCAACAGAGTGTGAAAGTCCCAAG | 2328 |
| Oy | 121 | CTCCCCAGCAGGCAAGATATGCAAAAGCATGTCACTTCAATTTAGTCAGCAACCATATGTCC | 180 |
| Db | 2327 | CTCCCCACACAGGCAAGATATGCAAAAGCATGTCACTTCAATTTAGTCAGCAACCATATGTCC | 2268 |
| Oy | 181 | GCCCCCTTA CTCGGCCATCCCGCCCTTAATCTCCGCCAGTTCCGCCCAATTCGCCGCCCA | 240 |
| Db | 2267 | GCCCCCTTA CTCGCCATCCCGCCCTTAATCTCCGCCAGTTCCGCCCAATTCGCCCTCA | 2208 |
| Oy | 241 | TGGCTGACTMAATTTTTTTTATTTATGACAGAGGCCGAGGCCCGCTCGGCTCTGAGCTATT | 300 |
| Db | 2207 | TCG-----TTCAAGTCTCTTAATTT-----TTCAAGTCTCTTAATTT | 2187 |
| Oy | 301 | CCAGAAATATGAGGAGGCTTTTTTTGAGGCCCTAGCCTTTTGCAAAAAGCTTACATGATC | 360 |
| Db | 2186 | TTACACACTTTGTAGAGGTTTTTACTTG----- | 2160 |
| Oy | 361 | TGCAGAGAGGCCACGATATACAGACTCTCTGACAGTCAATGGCGCTCACGACCTTTACAGCT | 420 |
| Db | 2159 | -----CTTTAAAAAAGCTCCACACCTCTCCCTGAACTGAAACCTAAATATGAA | 2111 |
| Oy | 421 | AGCCGTGACTAGGCGTAAATGAGTGCAGCCACCACTTAAAGAAAGGAAAGAAAGGAAAAA | 480 |
| Db | 2110 | TGCATATGTGTGTGTTAACTGTTTATGCACTTATATGTTTACAAATTAAGCAATATG | 20511 |
| Oy | 481 | AGAAAGAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA | 540 |
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| Oy | 541 | AA | 600 |
| Db | 1990 | ACTCATCATATGATCTTATCA-----TGTCGTCTGAAGC | 1956 |
| Oy | 601 | GAGCGGAGTGTATTAACCCCACTTAAACGGGATCTTTCGACCCTTCTTGAGCTTTATG | 660 |
| Db | 1955 | GAGCGGCGGCCCCGACCTAGAAATTAACAGGCGGATCTTTCGACCCTTCTTGAGCTTTATG | 1896 |
| Oy | 661 | AGGATCTCTGATTTTTCTTGCGTGAAGTTTTCCGATAGAAGCTTTGGATCTTCTGCTC | 720 |
| Db | 1895 | AGGATCTCTGATTTTTCTTGCGTGAAGTTTTCCGATAGAAGCTTTGGATCTTCTGCTC | 1836 |
| Oy | 721 | ACAAACACAACTCTTCGCGGCAACTTTTCGCGGTTGTTACTTGACTGCGACATGTAATCC | 780 |
| Db | 1835 | ACAAACACAACTCTTCGCGGCAACTTTTCGCGGTTGTTACTTGACTGCGACATGTAATCC | 1776 |
| Oy | 781 | AGGATCTCTTTTTTCCGTATGCTCTTTCGCGTCAAAACAAACAAAGCGCGCGGGAAGT | 840 |
| Db | 1775 | AGGATCTCTTTTTTCCGTATGCTCTTTCGCGTCAAAACAAACAAAGCGCGCGGGAAGT | 1716 |
| Oy | 841 | TCACCGGCGTATCGTCGGAAGACCTGCGACACACTGCGTGAAGATGTTGGGTTGTG | 900 |
| Db | 1715 | TCACCGGCGTATCGTCGGAAGACCTGCGACACACTGCGTGAAGATGTTGGGTTGTG | 1656 |
| Oy | 901 | AGCAAGATGATTTCCAAATTCAGCGGAGGACCTGATATGCTTTGTAATTAAGAGAC | 960 |
| Db | 1655 | AGCAAGATGATTTCCAAATTCAGCGGAGGACCTGATATGCTTTGTAATTAAGAGAC | 1596 |
| Oy | 961 | TTACAGGCGGTCAAGATGAAGAAGTGTGCTTGTCCAGTAAAGTATATCTCCAGAA | 1020 |
| Db | 1595 | TTACAGGCGGTCAAGATGAAGAAGTGTGCTTGTCCAGTAAAGTATATCTCCAGAA | 1536 |
| Oy | 1021 | TGTAGCATTCATCTCTTGATCATCAAGGCGTTGGTCCGCTCCGATGTTTATCAATACG | 1080 |
| Db | 1535 | TGTAGCATTCATCTCTTGATCATCAAGGCGTTGGTCCGATGTTTATCAATACG | 1476 |
| Oy | 1081 | GACATTAATCATATGACCTCTCAACACAGTTGCGCTCTTTGATTTAACGCCAGGCTTTTC | 1140 |
| Db | 1475 | GACATTAATCATATGACCTCTCAACACAGTTGCGCTCTTTGATTTAACGCCAGGCTTTTC | 1416 |

| | | | |
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| QY | 1141 | CCGGATTCAGATCCACACTTCGCTTCAAAAAATGGAACAATTTCACGACCGCGCC | 1200 |
| DB | 1415 | CCGGATTCAGATCCACACTTCGCTTCAAAAAATGGAACAATTTCACGACCGCGCC | 1356 |
| QY | 1201 | GGTTTATCA TCCCTCGGGGTGTAATGAA TACTGATGATCTGAGAGCCATAT | 1260 |
| DB | 1355 | GGTTTATATCCCCCTCGGGGTGTAATGAA TACTGATGATCTGAGAGCCATAT | 1296 |
| QY | 1261 | CCTTGCCGATACCTGGCAGATGGAACCTCTTGGCAACCGCTTCCCGACTTCTTAG | 1320 |
| DB | 1295 | CCTTCCGATACCTGGCAGATGGAACCTCTTGGCAACCGCTTCCCGACTTCTTAG | 1236 |
| QY | 1321 | AGGGAGCGCACCAAGAACATTTCTGTAAATTGATTAATCGTATTTGTCAATCAGA | 1380 |
| DB | 1235 | AGGGAGCGCACCAAGAACATTTCTGTAAATTGATTAATCGTATTTGTCAATCAGA | 1176 |
| QY | 1381 | GTGCTTTTGGGAAAGAAAGAAATAGGGTTGGCACAGCAGCGGACTTTGAATCTTGTA | 1440 |
| DB | 1175 | GTGCTTTTGGGAAAGAAAGAAATAGGGTTGGCACAGCAGCGGACTTTGAATCTTGTA | 1116 |
| QY | 1441 | TCCTGAAGGCTCTCAGAAAAGGCTCTTCAATCTATACATTAAGAACAATCGAAT | 1500 |
| DB | 1115 | TCCTGAAGGCTCTCAGAAAAGGCTCTTCAATCTATACATTAAGAACAATCGAAT | 1056 |
| QY | 1501 | CCACATATCAATATTCGAGTGTGTAAACAATTCGAAAACCGTATGGAATGGAACA | 1560 |
| DB | 1055 | CCACATATCAATATTCGAGTGTGTAAACAATTCGAAAACCGTATGGAATGGAACA | 996 |
| QY | 1561 | CTTAAATTCGAGTATCCGGAATGATTTGATTCGCAAAATATAGATCTCTGGCATTCGAG | 1620 |
| DB | 995 | CTTAAATTCGAGTATCCGGAATATTTGATTCGCAAAATATAGATCTCTGGCATTCGAG | 936 |
| QY | 1621 | AATCAGCGGAGGAGTTTATGAGGAGACGACCTTTAGGACAGCCAGTATCCA | 1680 |
| DB | 935 | AATCAGCGGAGGAGTTTATGAGGAGACGACCTTTAGGAGACAGTATGATCCA | 876 |
| QY | 1681 | GAGAGTTCATGATCAGTCAATGCTGTCTGTCCCTATCGAAGGACTCTGGCACAAAATCG | 1740 |
| DB | 875 | GAGAGTTCATGATCAGTCAATGCTGTCTGTCCCTATCGAAGGACTCTGGCACAAAATCG | 816 |
| QY | 1741 | TATTCATTTAAACCGGAGGTAGATGAGATGACGAACGTGTACATCGACTGAATCCC | 1800 |
| DB | 815 | TATTCATTTAAACCGGAGGTAGATGAGATGACGAACGTGTACATCGACTGAATCCC | 756 |
| QY | 1801 | TGCTATCCGCTTTAGAAATCCATGATTAATTTTTGGATGATGGAGCTTTTTTTC | 1860 |
| DB | 755 | TGCTATCCGCTTTAGAAATCCATGATTAATTTTTGGATGATGGAGCTTTTTTTC | 696 |
| QY | 1861 | ACGTTCAAAATTTTTTGGCAACCCCTTTTGGAAACGAACACACGATAGGCTGGAAATG | 1920 |
| DB | 695 | ACGTTCAAAATTTTTTGGCAACCCCTTTTGGAAACGAACACACGATAGGCTGGAAATG | 636 |
| QY | 1921 | CCCATCTGTGAGCAATTCAGTTCAATTATAAATGTCTTCGGGGCGCAATGCACT | 1980 |
| DB | 635 | CCCATCTGTGAGCAATTCAGTTCAATTATAAATGTCTTCGGGGCGCAATGCACT | 576 |
| QY | 1981 | CCGATTAATAACCGGCCCAACAACCGGCAATAAGATTTGAAGAGTTTCACTGCAATAG | 2040 |
| DB | 575 | CCGATTAATAACCGGCCCAACAACCGGCAATAAGATTTGAAGAGATTTTCACTGCAATAG | 516 |
| QY | 2041 | ACGATTCCTGTATTTGTAATTCAGGCCCATATGTTCAATAGCTTTCGCAACCGAAGGAC | 2100 |
| DB | 515 | ACGATTCCTGTATTTGTAATTCAGGCCCATATGTTTCAATAGCTTTCGCAACCGAAGGAC | 456 |
| QY | 2101 | ATTTGGAAGTCTCAGCGTAAAGTATGCACTCGATATGTGCATCTGTAAAGCAATT | 2160 |
| DB | 455 | ATTTGGAAGTCTCAGCGTAAAGTATGCACTCGATATGTGCATCTGTAAAGCAATT | 396 |
| QY | 2161 | GTTCCAGGAACCAAGGGGATCTCTTCAATAGCCTTATAGCACTTCTCCACGGTTCGA | 2220 |
| DB | 395 | GTTCCAGGAACCAAGGGGATCTCTTCAATAGCCTTATAGCACTTCTCCACGGTTCGA | 336 |

| | | | |
|----|------|---|------|
| OY | 841 | CCACGGCGTCATCGTCGGGAAAGACCTGCGACACCTGGCTGGAAGATGTTGGGGTGTTCG | 900 |
| Db | 1715 | TCACCGCGCTATCGTCGGGAAAGACCTGCGACACCTGGCTGGAAGATGTTGGGGTGTTCG | 1656 |
| OY | 901 | AGCAAGATGATTCCTCAATTCAGCGGGACCACTGATAGCCTTTGTACTTAATCAGAGAC | 960 |
| Db | 1655 | AGCAAGATGATTCCTCAATTCAGCGGGACCACTGATAGCCTTTGTACTTAATCAGAGAC | 1596 |
| OY | 961 | TTCAAGCGCGTCAACGATGAGAAGTGTTCGTTCTTGTCCTCAAGTAAGCTATGTCTCAGAA | 1020 |
| Db | 1595 | TTCAAGCGCGTCAACGATGAGAAGTGTTCGTTCTTGTCCTCAAGTAAGCTATGTCTCAGAA | 1536 |
| OY | 1021 | TGTAGCCATCCATCCTTGTCATCAAGGCGTTGGTCGTCGCTCCGAGTTGTTACATPAACG | 1080 |
| Db | 1535 | TGTAGCCATCCATCCTTGTCATCAAGGCGTTGGTCGTCGCTCCGAGTTGTTACATPAACG | 1476 |
| OY | 1081 | GACATTAATCATAGAGACCTCTCACACAGTTGCGCTCTTGATTTAACGCCAGCGTTC | 1140 |
| Db | 1475 | GACATTAATCATAGAGACCTCTCACACAGTTGCGCTCTTGATTTAACGCCAGCGTTC | 1416 |
| OY | 1141 | CCGGTATCCAGATCCACACCTTCGCTTCAAAAAATGGAACAATTNACGACCGCGCC | 1200 |
| Db | 1415 | CCGGTATCCAGATCCACACCTTCGCTTCAAAAAATGGAACAATTNACGACCGCGCC | 1356 |
| OY | 1201 | GCTTATATATCCCCCTCGGGGTGTATCAGATAGCTGATGTATGTCTAGTAGGCCATAT | 1260 |
| Db | 1355 | GCTTATATATCCCCCTCGGGGTGTATCAGATAGCTGATGTATGTCTAGTAGGCCATAT | 1296 |
| OY | 1261 | CCTTGCCGTATACCTGGGAGATGGAACCTCTTGCGCACCGCTCCCGCACCTTCCTTAGAG | 1320 |
| Db | 1295 | CCTTGCCGTATACCTGGGAGATGGAACCTCTTGCGCACCGCTTCGCCACCTTCCTTAGAG | 1236 |
| OY | 1321 | AGGGAGCGCCACGAGAACATTTTGGTAAATTGATTAATCGTATTTGTCAATCAG | 1380 |
| Db | 1235 | AGGGAGCGCCACGAGAACATTTTGGTAAATTGATTAATCGTATTTGTCAATCAG | 1176 |
| OY | 1381 | GTCGCTTTGGGGAAGAGAGATATAGGTTGGCACACGACGCACTTGAATCTTGTA | 1440 |
| Db | 1175 | GTCGCTTTGGGGAAGAGAGATATAGGTTGGCACACGACGCACTTGAATCTTGTA | 1116 |
| OY | 1441 | TCCGGAAGGCTCCTCAGAAACAGCTCTTCAATCTATPACATTAAGACACTCGAAT | 1500 |
| Db | 1115 | TCCGGAAGGCTCCTCAGAAACAGCTCTTCAATCTATPACATTAAGACACTCGAAT | 1056 |
| OY | 1501 | CCACATATCAATATCCGAGTGTAGTAACAATCCAAAAACGTCGATGGAATGGAACA | 1560 |
| Db | 1055 | CCACATATCAATATCCGAGTGTAGTAACAATCCAAAAACGTCGATGGAATGGAACA | 996 |
| OY | 1561 | CTTAAATCGCAGTATCCGGAATGATTTGATTCGCAAAATATAGATCTCTGCACTGCAG | 1620 |
| Db | 995 | CTTAAATCGCAGTATCCGGAATGATTTGATTCGCAAAATATAGATCTCTGCACTGCAG | 936 |
| OY | 1621 | AATCTCAGCGGAGCTTCTATGAGGCAACGACACTTTAAGCAGACGATGATTC | 1680 |
| Db | 935 | AATCTCAGCGGAGCTTCTATGAGGCAACGACACTTTAAGCAGACGATGATTC | 876 |
| OY | 1681 | GAGAGTTCATGATCAGTGCATTTGCTGTTGCCCATCGAAGACTCTGGCAAAAATCG | 1740 |
| Db | 875 | GAGAGTTCATGATCAGTGCATTTGCTGTTGCCCATCGAAGACTCTGGCAAAAATCG | 816 |
| OY | 1741 | TATTCATTAAACCGGGAGGTAGATGAGATGTGACGAACGTGTACATCGACTGAATCC | 1800 |
| Db | 815 | TATTCATTAAACCGGGAGGTAGATGAGATGTGACGAACGTGTACATCGACTGAATCC | 756 |
| OY | 1801 | TGCTAATCCGTTTGAATCCATGATTAATTTTGGATGATTTGGAGCTTTTTC | 1860 |
| Db | 755 | TGCTAATCCGTTTGAATCCATGATTAATTTTGGATGATTTGGAGCTTTTTC | 696 |
| OY | 1861 | ACGTTCAAAATTTTTCGACCCCTTTTGGAAACGAACACACGCTGAGCTGCGAAATG | 1920 |
| Db | 695 | ACGTTCAAAATTTTTCGACCCCTTTTGGAAACGAACACACGCTGAGCTGCGAAATG | 636 |
| OY | 1921 | CCCATACTGTTGAGCAATTCAGCTTCAATTAATGTGCTTCGCGGCGCACTGCAACT | 1980 |

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| Db | 635 | CCCACTACTGTTGAGCAATTCACGTTCACTATTATAATGTCGTTCCGGGGCGCAACTGCAACT | 576 |
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| Db | 515 | ACGATTTCTGATTTTGTATTCACGCCCATATCGTTTCTTACCTTCTGCAACCGAAGCGAG | 456 |
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| Db | 455 | ATTTCGAAGTACTCAGCGGTAAAGTATGCCACCTCGATATGTGCATCTGTAAAGCAATT | 396 |
| Qy | 2161 | GTTCACAGAAACAGAGGGCGTATCTTTTCATAGACCTTATGACAGTTGCTCTCCAGCGGTTCA | 2220 |
| Db | 395 | GTTCACAGAAACAGAGGGCGTATCTTTTCATAGACCTTATGACAGTTGCTCTCCAGCGGTTCA | 336 |
| Qy | 2221 | TCTTCACGCGGATATGATGCGCGCGGCGCTTTCTTATGTTTTTGGGCGCTTCCATATGG | 2278 |
| Db | 335 | TCTTCACGCGGATATGATGCGCGCGGCGCTTTCTTATGTTTTTGGGCGCTTCCATATGG | 278 |
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| ACCESSION | AF416988 | | |
| VERSION | AF416988.1 | GI:17530178 | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | 1. (bases 1 to 6612) | | |
| TITLE | Amarszuicui,M., Brede,G., Babaie,E., Grotti,M., Sprout,B. and Prydz,H. | | |
| JOURNAL | Secondary structure prediction and in vitro accessibility of mRNA | | |
| MEDLINE | Nucleic Acids Res. 28 (21), 4113-4124 (2000) | | |
| PUBMED | 20512557 | | |
| REFERENCE | 11058107 | | |
| AUTHORS | 2 (bases 1 to 6612) | | |
| TITLE | Amarszuicui,M., Holten,T. and Prydz,H.P.B. | | |
| JOURNAL | Direct Submission | | |
| FEATURES | Submitted (07-SEP-2001) The Biotechnology Centre of Oslo, University of Oslo, Gaustadalleen 21, Oslo 0373, Norway | | |
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ORIGIN

Query Match 63.6%; Score 1763.2; DB 12; Length 6612;
Best Local Similarity 87.9%; Pred. No. 0;
Matches 2002; Conservative 0; Mismatches 168; Indels 108; Gaps 3;

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 ACCESSION CQ803129.1 GI:47110086
 VERSION CQ803129.1 GI:47110086
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 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
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 AUTHORS Seibler, J., Schwenk, F., Kuehn, R. and Kueter-Luke, B.
 TITLE Sirtin mediated gene silencing in transgenic animals
 JOURNAL Patent: WO 2004035782-A 15 29-APR-2004;
 ARTEMIS Pharmaceuticals GmbH (DE)
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RESULT 14

AX528380
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ACCESSION AX528380
VERSION AX528380.1 GI:25172613
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AUTHORS
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Best Local Similarity 87.9%; Pred. No. 0;
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 SOURCE
 ORGANISM
 other sequences; artificial sequences.
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 AUTHORS Oman, C.S., Olde, B.A. and Kotarsky, K.
 TITLE Reporter system for cell surface receptor-ligand binding
 JOURNAL Patent: WO 0220749-A 12 14-MAR-2002;
 Oman, Christer S. D. (SE) ; Olde, Bjorn A. (SE) ; Kotarsky, Knut (SE)

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 Qy 66 GATATCAAGATGATGATCAATTTAGTACGACACGAGTGTGAAGTCCCGAGCTCC 125
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 Qy 126 CAGCAGCAGAGATGAGAAAGCATGCTCAATTAATGACGACCAATAGTCCGCCCC 185
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| OY | 486 | GAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG | 545 |
| Db | 410 | CAAAATTCACAAATTAAGCAATTTTTTTCACATGATCTTATGTTGTGTTTTCACAACTCA | 469 |
| OY | 546 | AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAAATGGCTTAAAGGCG | 605 |
| Db | 470 | TCAATGTATCTTATCA-----TGTGTCTCGAAGGGGCG | 504 |
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| OY | 966 | GCGGTCAAGATGAAGAAGTGTGCTCTTTCGTCAGTAACTATGTCACAGATGTAG | 1025 |
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| OY | 1026 | CCATTCATCTTTGTCAATCAAGGGCGTGTGCTTCGGGATTTGTTTACATAACCGGACAT | 1085 |
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| OY | 1325 | GAGCGCCACCGAAGCAATTTCTGTGTAATTAATGATTAATGCTATTTGTCAATCAGAGTC | 1384 |
| Db | 1225 | GAGCGCCACCGAAGCAATTTCTGTGTAATTAATGATTAATGCTATTTGTCAATCAGAGTC | 1284 |
| OY | 1385 | TTTTGGCGAAGAAGAAATAGAGTTGGCAACGACGACGACTTTGAACTGTGAAATCCT | 1444 |
| Db | 1285 | TTTTGGCGAAGAAGAAGAAATAGAGTTGGCAACGACGACGACTTTGAACTGTGAAATCCT | 1344 |
| OY | 1445 | GAAAGCTCTTCAGAAACAGCTCTTCTTCAATCTATACATTAAGACGACTCGAAATCCAC | 1504 |
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| OY | 1865 | TCAAAATTTTTTGGAAACCCCTTTTGGAAAGAAACACACAGATAGGTGGGAAATGCGCA | 1924 |
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| OY | 1985 | TAAATTAACGGGCCCAACACGGGCAATAAGAAATGAAGAGTTTTCCTCATATACGACGA | 2044 |
| Db | 1885 | TAAATTAACGGGCCCAACACGGGCAATAAGAAATGAAGAGTTTTCCTCATATACGACGA | 1944 |
| OY | 2045 | TTCTGTATTTGTATTCAGCCCATATCGTTTCATAGCTTGTGCAACCGAACGACATTT | 2104 |
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| Db | 2005 | CGAAGTACTCAGCGTAAATGATGTGCCCTTCGATATGTGCATCTGTAAAGCAATTTGTC | 2064 |
| OY | 2165 | CAGGAACCAAGGCGTATCTTTCATATAGCCTTAATAGAGTTGCTCTCAGCGGTTCCATCTT | 2224 |
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| Db | 2125 | CCAGCGGATAGATAGCGCGCGGCTTTCTTTATGTTTTGGCGTCTTCCATAG | 2178 |

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OM nucleic - nucleic search, using sw model

Run on: September 29, 2005, 11:18:45; Search time 1436 Seconds
(without alignments)
11423.122 Million cell updates/sec

Title: US-10-734-801-18

Perfect score: 2771

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 3 | 2674 | 96.5 | 2674 | 6 | ABQ78073 |
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| 5 | 1763.2 | 63.6 | 5064 | 6 | AAAD27538 |
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| 8 | 1763.2 | 63.6 | 7014 | 12 | ADN11354 |
| 9 | 1758.2 | 63.5 | 7788 | 6 | ADN11354 |
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| 11 | 1663.4 | 60.0 | 11004 | 12 | ADN11354 |
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| 18 | 1657.6 | 59.8 | 5010 | 13 | ADR72550 |
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| C | 23 | 1657.6 | 59.8 | 5960 | 2 | AAV45225 | AAV45225 Human ner |
| C | 24 | 1657.6 | 59.8 | 5982 | 13 | AD575092 | Ad575092 Plasmid p |
| C | 25 | 1657.6 | 59.8 | 8307 | 13 | ADQ91241 | Adq91241 Expressio |
| C | 26 | 1657.6 | 59.8 | 8763 | 10 | ACF04645 | ACF04645 Vector co |
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| C | 38 | 1655 | 59.7 | 12850 | 4 | AAAD07495 | AAAD07495 pZEO1P+lu |
| C | 39 | 1654.4 | 59.7 | 4824 | 4 | AAAD10009 | AAAD10009 Plasmid p |
| C | 40 | 1654.2 | 59.7 | 7460 | 4 | AAH74867 | AAH74867 Nucleoid |
| C | 41 | 1654.2 | 59.7 | 14194 | 4 | AAAC6632 | AAAC6632 Plant sig |
| C | 42 | 1653.4 | 59.7 | 1706 | 13 | ADR12256 | ADR12256 Luciferas |
| C | 43 | 1653.4 | 59.7 | 2477 | 6 | ABT07352 | ABT07352 Reporter |
| C | 44 | 1653.4 | 59.7 | 2477 | 10 | ADFA9175 | ADFA9175 Luciferas |
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ALIGNMENTS

| | |
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| RESULT 1 | ABQ78072 standard; DNA; 2771 BP. |
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| XX | ABQ78072; |
| AC | 30-OCT-2002 (first entry) |
| XX | |
| DT | Partial PMJ050 construct SEQ ID NO 18. |
| XX | |
| DE | Genomic replication; RNA-dependent RNA polymerase virus; RDRP virus; |
| XX | infection; ds. |
| KW | Rheus macaque polyoma virus. |
| OS | Hepatitis C virus. |
| OS | Hepatitis D virus. |
| OS | Unidentified. |
| XX | Chimeric. |
| XX | |
| PH | Key |
| FT | promoter |
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| XX | |
| XX | WO200261048-A2. |
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| XX | 08-AUG-2002. |
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| XX | 31-JAN-2002; 2002WO-US002952. |


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DB 1981 CCGATTAATTAACCGGCGCCCAACCGGCGATTAAGAAATTAAGAGAGTTTCACTGCAATG 2040
QY 2041 ACGATTTCTGATTTGATTTAGATTCAGCCCAATGCTTCAATGCTTCCCAACCGGAGC 2100
DB 2041 ACGATTTCTGATTTGATTTAGATTCAGCCCAATGCTTCAATGCTTCCCAACCGGAGC 2100
QY 2101 ATTTGGAAGTACTCAGCGTAAGTGAATGTCACCTCGATATGTCATCTGTAAAGCAAT 2160
DB 2101 ATTTGGAAGTACTCAGCGTAAGTGAATGTCACCTCGATATGTCATCTGTAAAGCAAT 2160
QY 2161 GTTCCAGGAAACCGGCGCGTATCTTCAATAGCTTATGCAAGTTGCTCTCCAGCGTTCA 2220
DB 2161 GTTCCAGGAAACCGGCGCGTATCTTCAATAGCTTATGCAAGTTGCTCTCCAGCGTTCA 2220
QY 2221 TCTTCAGGAGTAAATGAGCGCGGCGCTTCTTAATGTTTGGCGCTTCCATGAGGA 2280
DB 2221 TCTTCAGGAGTAAATGAGCGCGGCGCTTCTTAATGTTTGGCGCTTCCATGAGGA 2280
QY 2281 CGTCGCTTGTGTTAGCTTGTGTTTCTTTGAGGTTTGAATGTCGTCATGATGAC 2340
DB 2281 CGTCGCTTGTGTTAGCTTGTGTTTCTTTGAGGTTTGAATGTCGTCATGATGAC 2340
QY 2341 GGTCTACGAGACTCTCCGGGCGACTCGCAAGCACTTACAGGAGTACCAAGGCTT 2400
DB 2341 GGTCTACGAGACTCTCCGGGCGACTCGCAAGCACTTACAGGAGTACCAAGGCTT 2400
QY 2401 TCGGAGCCCAACACTACCTGCTAGCACTTGCAGGCGGCGAGCCCAATCTCCAGGCA 2460
DB 2401 TCGGAGCCCAACACTACCTGCTAGCACTTGCAGGCGGCGAGCCCAATCTCCAGGCA 2460
QY 2461 TGAGCGGGTTATCTCAAGAAAGAACCCGCTCGTCCGCAATTCGCGTACTACCGGT 2520
DB 2461 TGAGCGGGTTATCTCAAGAAAGAACCCGCTCGTCCGCAATTCGCGTACTACCGGT 2520
QY 2521 TCCGAGACCACTAATGCTCTCCCGGAGGCGGCTCTGAGGCTGACGACACTCAT 2580
DB 2521 TCCGAGACCACTAATGCTCTCCCGGAGGCGGCTCTGAGGCTGACGACACTCAT 2580
QY 2581 CTAAAGCCATGCTAGAGCTTTCTGCGGAGAGACAGATGTTCCACAGGGGAGATG 2640
DB 2581 CTAAAGCCATGCTAGAGCTTTCTGCGGAGAGACAGATGTTCCACAGGGGAGATG 2640
QY 2641 CATGCTGAGTGTGCTCCCATCAGGGGCTGGCGCGGCAATGATCCAGCTCTCTGC 2700
DB 2641 CATGCTGAGTGTGCTCCCATCAGGGGCTGGCGCGGCAATGATCCAGCTCTCTGC 2700
QY 2701 TGGCGCCGCTGGGCAACATTCGAGGAGGACCGTCTCGGTAAATGCGAAATGAGACCC 2760
DB 2701 TGGCGCCGCTGGGCAACATTCGAGGAGGACCGTCTCGGTAAATGCGAAATGAGACCC 2760
QY 2761 ACAATCTCTC 2771

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DB 2761 ACAATCTCTC 2771

RESULT 2
ID ABQ78071 standard; DNA; 5860 BP.
XX
AC ABQ78071;
XX
DT 30-OCT-2002 (first entry)
XX
DE pm050 construct SEQ ID NO 17.
XX
KM Genomic replication; RNA-dependent RNA polymerase virus; RDRP virus;
XX infection; ds.
XX
OS Rhesus macaque polyoma virus.
XX
OS Hepatitis C virus.
XX
OS Hepatitis D virus.
XX
OS Unidentified.
XX
OS Synthetic.
XX
OS Chimeric.
XX
FH Key
FT 1. 347
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FT 3'UTR
FT /tag= b
FT /note= "Hepatitis C virus 3'UTR, antisense orientation"
FT misc_feature
FT /tag= c
FT /note= "Luciferase sequence, antisense orientation"
FT 5'UTR
FT /tag= d
FT /note= "Hepatitis C virus 5'UTR, antisense orientation"
FT RBS
FT /tag= e
FT /note= "Hepatitis delta virus ribozyme sequence, sense
FT /note= "Hepatitis delta virus ribozyme sequence, sense
FT /tag= f
FT /note= "pm050 plasmid backbone sequence"

WO200261048-A2.
08-AUG-2002.
31-JAN-2002; 2002WO-US002952.
PR 31-JAN-2001; 2001US-0265437P.
PA (BRIS-) BRISTOL MYERS SQUIBB PHARMA CO.
PI King RW, Jeffries MW, Paquinelli C;
XX
DR WPI; 2002-619240/66.
XX
PT Measuring the genomic replication of RNA-dependent RNA polymerase (RDRP)
PT virus, for designing therapies for the treatment of cells infected with
PT RDRP viruses, by transfecting cultured cells with a construct comprising
PT the cDNA.
XX
PS Example 1; Fig 3; 60bp; English.
XX
CC The invention relates to methods for measuring the genomic replication of
CC a virus that is dependent for replication upon RNA-dependent RNA
CC polymerase (RDRP) virus comprising transfecting cells with a construct
CC having, in antisense orientation, the cDNA of a reporter gene sequence
CC operably linked on its 5' end with the untranslated region (UTR) of the
CC native 3' end of the RDRP virus and operably linked on its 3' end with
CC the UTR of the native 5' end of the RDRP virus. The methods are useful

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```

Db      1981 CCGATAAATAAGCGCCCAACACCGGCATAAAGATTGAAGAGTTCCTACGTCATAGC 2040
Qy      2041 ACGATTCTGTGATTTTGTATTCAGCCCAATCGTTTCATAGCTTCTGCGCAACGGAACGAGC 2100
Db      2041 ACGATTCTGTGATTTTGTATTCAGCCCAATCGTTTCATAGCTTCTGCGCAACGGAACGAGC 2100
Qy      2101 ATTTGGAATCTACGACGCTAGATGATGTCACCTGATATGTCATCTGTAAGCAAT 2160
Db      2101 ATTTGGAATCTACGACGCTAGATGATGTCACCTGATATGTCATCTGTAAGCAAT 2160
Qy      2161 GTTCCAGAACGAGCGGCTATCTCTCATAGCCTTATGCAAGTTGCTCTCAGCGGTTTCCA 2220
Db      2161 GTTCCAGAACGAGCGGCTATCTCTCATAGCCTTATGCAAGTTGCTCTCAGCGGTTTCCA 2220
Qy      2221 TCTTCCAGCGGATAGATGAGCGCGGCGCTTCTTTATGTTTGGCGTCTTCATGGGA 2280
Db      2221 TCTTCCAGCGGATAGATGAGCGCGGCGCTTCTTTATGTTTGGCGTCTTCATGGGA 2280
Qy      2281 CGTCGGTGTGTAGTGTGTTTCTTTGAGGTTTGAAGTTGTCGTCATGATGAC 2340
Db      2281 CGTCGGTGTGTAGTGTGTTTCTTTGAGGTTTGAAGTTGTCGTCATGATGAC 2340
Qy      2341 GGTCTACGAGACCTCCCGGCGCACTGCAAGCACCTTATCAGGACATACCAAGGCTT 2400
Db      2341 GGTCTACGAGACCTCCCGGCGCACTGCAAGCACCTTATCAGGACATACCAAGGCTT 2400
Qy      2401 TCGCGACCCCAACTACTCGGCTAGAGTCTTTCGGGGGCGACGCCAAATCTCCAGGCAT 2460
Db      2401 TCGCGACCCCAACTACTCGGCTAGAGTCTTTCGGGGGCGACGCCAAATCTCCAGGCAT 2460
Qy      2461 TGAAGCGGGGTATTCGAAGAAAGAACCCGCGTCCGTCGCAATTCGGGTACACCGGT 2520
Db      2461 TGAAGCGGGGTATTCGAAGAAAGAACCCGCGTCCGTCGCAATTCGGGTACACCGGT 2520
Qy      2521 TCGCGACCACTATGAGTCTCCCGGAGGCGGCTCTGAGAGGCTGCAACACTCAT 2580
Db      2521 TCGCGACCACTATGAGTCTCCCGGAGGCGGCTCTGAGAGGCTGCAACACTCAT 2580
Qy      2581 CTAAAGCCATGCTAGACGCTTCTGCGTGAAGACAGTATGCTTCAACAGGGAGTAT 2640
Db      2581 CTAAAGCCATGCTAGACGCTTCTGCGTGAAGACAGTATGCTTCAACAGGGAGTAT 2640
Qy      2641 CATGTGAGAGTGTGCGCCCATCAGAGGCGCTGCGGCGGCGCATGTCACGCTCTCCG 2700
Db      2641 CATGTGAGAGTGTGCGCCCATCAGAGGCGCTGCGGCGGCGCATGTCACGCTCTCCG 2700
Qy      2701 TGGCGCGGCTGGGCAACATTCGAGAGGAGCGTCCCTCGGTAATGGCAATGGAGCC 2760
Db      2701 TGGCGCGGCTGGGCAACATTCGAGAGGAGCGTCCCTCGGTAATGGCAATGGAGCC 2760
Qy      2761 ACAAAATCTCTC 2771
Db      2761 ACAAAATCTCTC 2771

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FH      Key      Location/Qualifiers
FT      Promoter      1..347
FT      3'UTR      /tag= a
FT      /note= "SV40_promoter"
FT      /tag= b
FT      /note= "Hepatitis C virus 3'UTR, antisense orientation"
FT      misc_feature      627..2284
FT      /tag= c
FT      /note= "Luciferase sequence, antisense orientation"
FT      5'UTR      2285..2674
FT      /tag= d
FT      /note= "Hepatitis C virus 5'UTR, antisense, orientation"
PN      WO200261048-A2.
PD      08-AUG-2002.
PF      31-JAN-2002; 2002WO-US002952.
PR      31-JAN-2001; 2001US-0265437P.
XX      (Bris-) BRISTOL MYERS SQUIBB PHARMA CO.
XX      King RW, Jeffries MW, Pasquonelli C;
XX      WPI; 2002-619240/66.
XX      Measuring the genomic replication of RNA-dependent RNA polymerase (RDRP)
XX      viruses, for designing therapies for the treatment of cells infected with
XX      RDRP viruses, by transfecting cultured cells with a construct comprising
XX      the cDNA.
XX      Example 1; Fig 3; 60pp; English.
XX      The invention relates to methods for measuring the genomic replication of
XX      a virus that is dependent for replication upon RNA-dependent RNA
XX      polymerase (RDRP) virus comprising transfecting cells with a construct
XX      having, in antisense orientation, the cDNA of a reporter gene sequence
XX      operably linked on its 5' end with the untranslated region (UTR) of the
XX      native 3' end of the RDRP virus and operably linked on its 3' end with
XX      the 5'UTR of the native 5' end of the RDRP virus. The methods are useful
XX      for designing therapies for the in vivo treatment of cells that are
XX      infected with RDRP viruses. The methods are also useful to provide a
XX      convenient platform for screening inhibitors to RDRP viral replication.
XX      The present sequence is that of part of the pm050 construct (AB078071)
XX      used in examples of the invention
XX      Sequence 2674 BP; 735 A; 665 C; 622 G; 652 T; 0 U; 0 Other;
XX
Qy      Query Match      96.5%; Score 2674; DB 6; Length 2674;
Qy      Best Local Similarity 100.0%; Pred. No. 0;
Qy      Matches 2674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GGAATCCGCTGAGATGCTGTCTAGTGGGTGGAAGTCCAGGCTCCCGACGAG 60
Db      1 GGAATCCGCTGAGATGCTGTCTAGTGGGTGGAAGTCCAGGCTCCCGACGAG 60
Qy      61 CAGAAGTATGACAAGCATCATCTCAATTAGTCAGCAACAGAGTGTGAAGTCCCGAG 120
Db      61 CAGAAGTATGACAAGCATCATCTCAATTAGTCAGCAACAGAGTGTGAAGTCCCGAG 120
Qy      121 CTCCCGACGAGCAGAAAGTATGCAATGATGATGATGATGATGATGATGATGAT 180
Db      121 CTCCCGACGAGCAGAAAGTATGCAATGATGATGATGATGATGATGATGATGAT 180
Qy      181 GCGCCCTAATCTCGGCGCATCCGCGCTCACTCGGCGCGGCTGCGGCGCATTCGCGCCCA 240
Db      181 GCGCCCTAATCTCGGCGCATCCGCGCTCACTCGGCGCGGCTGCGGCGCATTCGCGCCCA 240
Qy      241 TGGCTACTAATTTTATTTATTTATGAGAGGCGGCGGCTGCGGCTGAGGTAT 300
Db      241 TGGCTACTAATTTTATTTATTTATGAGAGGCGGCGGCTGCGGCTGAGGTAT 300

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DB 301 CCAAGAGTAGAGAGGCTTTTGGAGGCTTGGAGGCTTTTGGAAAAAGCTTACATGATC 360
QY 361 TGCAGAGAGGCACTATCAGCACTCTCTGAGTATGCGGCTCACGGACCTTTTCAAGCT 420
DB 361 TGCAGAGAGGCACTATCAGCACTCTCTGAGTATGCGGCTCACGGACCTTTTCAAGCT 420
QY 421 AGCGGTGACTAGGCTTAAGATGAGGCCACTTTAAAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 AGCGGTGACTAGGCTTAAGATGAGGCCACTTTAAAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 AGAAG 540
DB 481 AGAAG 540
QY 541 AAA 600
DB 541 AAA 600
QY 601 GGCAGAGTGTTCACCCCACTTTAAACGGCGATCTTTCCGCCCTTCTTGAGCTTTATG 660
DB 601 GGCAGAGTGTTCACCCCACTTTAAACGGCGATCTTTCCGCCCTTCTTGAGCTTTATG 660
QY 661 AGGATCTCTGATTTTCTTGCGTGAAGTTTCCGGTAAGACCTTTCCGACTTCTGCTCC 720
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QY 781 ACGATCTCTTTTCCGTCATGCTTTCGCTCCGTCGCAAAACAACAAGGCGCGGGAAGT 840
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QY 841 TCAACGGGCTGATGCTGCGGAGAGACTGCGACACTCGCGTGAAGATGTTGGGGTGTGG 900
DB 841 TCAACGGGCTGATGCTGCGGAGAGACTGCGACACTCGCGTGAAGATGTTGGGGTGTGG 900
QY 901 AGCAAGATGATTCCTCAATTCAGCGGAGCGCACTGATAGCTTTTGTAAATCAGAGAC 960
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QY 961 TTGAGGGGCTCAACAGAGAGAGAGTCTTCTGCTTCCGATAGCTATGCTCCAGAA 1020
DB 961 TTGAGGGGCTCAACAGAGAGAGAGTCTTCTGCTTCCGATAGCTATGCTCCAGAA 1020
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DB 1021 TGTAGCATCATCTTGTCAATCAAGGCGTTCGCTTCCGGAATGTTTACATAACCG 1080
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DB 1081 GACATAATCATAGGACCTCTCAACACAGTTCCGCTCTTTGATTAAAGCCCAAGGTTTC 1140
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DB 1141 CCGGTAATCAGATTCACAACTTCGCTTCAAAAAATGAAACAATTAAACCGACCGGCC 1200
QY 1201 GGTTCATCATCCCTCGGGTGTATCAGAAATAGCTATGATGCTCAGTGAAGCCATAT 1260
DB 1201 GGTTCATCATCCCTCGGGTGTATCAGAAATAGCTATGATGCTCAGTGAAGCCATAT 1260
QY 1261 CTTTGCCTGATACCTGCGAGATGAACTTTTGCGCAACCGCTTCCGACTTCTTAAAG 1320
DB 1261 CTTTGCCTGATACCTGCGAGATGAACTTTTGCGCAACCGCTTCCGACTTCTTAAAG 1320
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DB 1321 AGGGGAGCGGCAACAGAGAGATTTCTGTAAATTAATTAATTAATTAATTAATTAATTA 1380

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DB 1381 GTGCTTTTGGCAGAGAGAGAAATAGGCTTGGCAGCAGCGGCGCACTTTGAATCTTGTAA 1440
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DB 1441 TCTGAAAGGCTCTCAGAAAACAGCTCTTCTCAAACTATATATTAAGAGACTCGAAAT 1500
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DB 1561 CTTAAATCCGATATCCGGAATGATTTGATTCGCAAAAATAGGATCTCGGATGCGAG 1620
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DB 1741 TATTCAATTAACACGGGAGGTAGATGATGACGAAAGTGTACATCGAAGAAATCC 1800
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DB 1801 TGGTAAATCCGTTTAAATCAATGATATATTTTGGATGATGAGGAGCTTTTGTTC 1860
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DB 1861 ACGTTCAAAATTTTGGCAACCCCTTTTGGAAAAGAAACAACGAGTACGCGGAAATG 1920
QY 1921 CCGATACGTGTGACAAATTCACCTTCAATTAATATGCTTCCGCGGCGCACTGCAACT 1980
DB 1921 CCGATACGTGTGACAAATTCACCTTCAATTAATATGCTTCCGCGGCGCACTGCAACT 1980
QY 1981 CCGATTAATTAACGCGGCCCAACCGGCAATTAAGAAATTTGAAGAGTTTCACTGATACG 2040
DB 1981 CCGATTAATTAACGCGGCCCAACCGGCAATTAAGAAATTTGAAGAGTTTCACTGATACG 2040
QY 2041 ACGATCTGATGATTTGATTAACGCGCATATCCGTTCAATAGCTTCCGCAACGAGAC 2100
DB 2041 ACGATCTGATGATTTGATTAACGCGCATATCCGTTCAATAGCTTCCGCAACGAGAC 2100
QY 2101 ATTTCGAAGTACTCAGCGTATGATGATCCACTCGATATGTCATCTGTAAAGCAATT 2160
DB 2101 ATTTCGAAGTACTCAGCGTATGATGATCCACTCGATATGTCATCTGTAAAGCAATT 2160
QY 2161 GTTCCAGAAACGAGGCGTATCTTTCATAGCTTATGCAATGCTCTCAGCGGTTCCA 2220
DB 2161 GTTCCAGAAACGAGGCGTATCTTTCATAGCTTATGCAATGCTCTCAGCGGTTCCA 2220
QY 2221 TCTTCCAGGGAATGATGCGCGGCGCTTCTTATATGTTTGGCGTCTTCCAGAGGA 2280
DB 2221 TCTTCCAGGGAATGATGCGCGGCGCTTCTTATATGTTTGGCGTCTTCCAGAGGA 2280
QY 2281 CGTCGGTGGTGTACGTTTGGTTTCTTGTAGAGTTTGAATTCGTGCTCATGATGAC 2340
DB 2281 CGTCGGTGGTGTACGTTTGGTTTCTTGTAGAGTTTGAATTCGTGCTCATGATGAC 2340
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DB 2341 GGTTCAGAGACCTCCCGGCGCACTGCGAAGCACTTATCAGGCACTCAACAGGCTTT 2400
QY 2401 TCGGGAACCAACATCTGCGCTAGAGAGTCTCGGCGGCGAGCCCAATCTCCAGGCAAT 2460
DB 2401 TCGGGAACCAACATCTGCGCTAGAGAGTCTCGGCGGCGAGCCCAATCTCCAGGCAAT 2460
QY 2461 TGAAGCGGGTTATCAAGAAAGAACCGGCTGCTGCAATTCGAGTATCAACGGGT 2520


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DB 2461 TGAGGGGGTTATTCAGAAAGAACCGGTCCTCGGCAATTCGGGTACTCACCGGT 2520
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DB 2521 TCCGAGACCACTATGCTCTCCCGGAGGGGGGCTCTGAGAGCTGCACGACTCATTA 2580
QY 2581 CTAAAGCCATGCTAGACGCTTCTGCGTGAAGACGATGTTCTTCACAGGGGAGTGAAT 2640
DB 2581 CTAAAGCCATGCTAGACGCTTCTGCGTGAAGACGATGTTCTTCACAGGGGAGTGAAT 2640
QY 2641 CATGTGAGTGTCCGCCCATCAGGGGAGCTGGC 2674
DB 2641 CATGTGAGTGTCCGCCCATCAGGGGAGCTGGC 2674

RESULT 4
ABQ78074
ID ABQ78074 standard; DNA; 2327 BP.
XX
XX ABQ78074;
XX
XX 30-OCT-2002 (first entry)
XX
XX Partial pm050 construct SEQ ID NO 20.
XX
XX Genomic replication; RNA-dependent RNA polymerase virus; RDRP virus;
XX infection; ds.
XX
XX Hepatitis C virus.
XX
XX OS
XX Chimeric.
XX
XX FH Location/Qualifiers
XX 3'UTR 1..279
XX FT /note= "Hepatitis C virus 3'UTR, antisense orientation"
XX FT /tag= b
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XX FT misc_feature
XX FT /tag= c
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XX FT 1938..2327
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XX FT /note= "Hepatitis C virus 5'UTR, antisense orientation"
XX
XX EN WO200261048-A2.
XX
XX PD 08-AUG-2002.
XX
XX PF 31-JAN-2002; 2002WO-US002952.
XX
XX PR 31-JAN-2001; 2001US-0265437P.
XX
XX PA (BRIS-) BRISTOL MYERS SQUIBB PHARMA CO.
XX
XX PI King RW, Jeffries MW, Pasquinelli C;
XX
XX WPI; 2002-619240/66.
XX
XX DR
XX
XX PT Measuring the genomic replication of RNA-dependent RNA polymerase (RDRP)
XX PT virus, for designing therapies for the treatment of cells infected with
XX PT RDRP viruses, by transfecting cultured cells with a construct comprising
XX PT the cDNA.
XX
XX PS Example 1; Fig 3; 60pp; English.
XX
XX CC The invention relates to methods for measuring the genomic replication of
XX CC a virus that is dependent for replication upon RNA-dependent RNA
XX CC polymerase (RDRP) virus comprising transfecting cells with a construct
XX CC having, in antisense orientation, the cDNA of a reporter gene sequence
XX CC operably linked on its 5' end with the untranslated region (UTR) of the
XX CC native 3' end of the RDRP virus and operably linked on its 3' end with
XX CC the UTR of the native 5' end of the RDRP virus. The methods are useful
XX CC for designing therapies for the in vivo treatment of cells that are

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CC infected with RDRP viruses. The methods are also useful to provide a
CC convenient platform for screening inhibitors to RDRP viral replication.
CC The present sequence is that of part of the pm050 construct (ABQ78071)
CC used in examples of the invention
XX
XX Sequence 2327 BP; 655 A; 562 C; 537 G; 573 T; 0 U; 0 Other;
XX
XX Query Match 84.0%; Score 2327; DB 6; Length 2327;
XX Best Local Similarity 100.0%; Pred. No. 1,1e-302; Mismatches 0; Gaps 0;
XX Matches 2327; Conservative 0; Indels 0;
XX
QY 348 AGCTTACATGATCTCTCAGAGAGCCGATATCAGCACTCTCTGCACTATGCGGCTCACGG 407
DB 1 AGCTTACATGATCTCTCAGAGAGCCGATATCAGCACTCTCTGCACTATGCGGCTCACGG 60
QY 408 ACCTTTACAGCTACCGCTGACTAGGCGCTAGATGAGGCCACATTAAAGAAAGAA 467
DB 61 ACCTTTACAGCTACCGCTGACTAGGCGCTAGATGAGGCCACATTAAAGAAAGAA 120
QY 468 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 527
DB 121 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 180
QY 528 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 587
DB 181 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 240
QY 588 AATAGGCTTAAGAGCCGGAAGTGTATACCCCACTTTAAACGGGATCTTCCGCCCT 647
DB 241 AATAGGCTTAAGAGCCGGAAGTGTATACCCCACTTTAAACGGGATCTTCCGCCCT 300
QY 648 CTTGGCCTTTATGAGGATCTCTGATTTTCTTGGGCGAGTTTCCGGTAAACCTTT 707
DB 301 CTTGGCCTTTATGAGGATCTCTGATTTTCTTGGGCGAGTTTCCGGTAAACCTTT 360
QY 708 CGGTACTTCGTCACAAACACAACTCTCCGCGCACTTTTCCGGGTTGTTACTTGA 767
DB 361 CGGTACTTCGTCACAAACACAACTCTCCGCGCACTTTTCCGGGTTGTTACTTGA 420
QY 768 GCGAGATATCAGATCTCTTTTCCGTCATGCTTTTCCGTCGTCACAAACAA 827
DB 421 GCGAGATATCAGATCTCTTTTCCGTCATGCTTTTCCGTCGTCACAAACAA 480
QY 828 GCGGCGGGAAGTTTCAACGGGCTCATGTCGGGAAGACTTGGGAGCACTGCGTGAAGT 887
DB 481 GCGGCGGGAAGTTTCAACGGGCTCATGTCGGGAAGACTTGGGAGCACTGCGTGAAGT 540
QY 888 GTTGGGGTGTGAGCAAGATGATTCATTCATTCAGCGGAGCACTGATAGCTTTTGA 947
DB 541 GTTGGGGTGTGAGCAAGATGATTCATTCATTCAGCGGAGCACTGATAGCTTTTGA 600
QY 948 CTTAATCAGAGACTTCAGGCGGTCAACGATGAAGAAGTGTGCTTGTCTCCAGTAAGC 1007
DB 601 CTTAATCAGAGACTTCAGGCGGTCAACGATGAAGAAGTGTGCTTGTCTCCAGTAAGC 660
QY 1008 TATGTCCTCAGATGTAGCATTCATCTTGTTCATCAAGGGTGTGCTTCCGGAT 1067
DB 661 TATGTCCTCAGATGTAGCATTCATCTTGTTCATCAAGGGTGTGCTTCCGGAT 720
QY 1068 GTTACATTAACCGGACATATATATAGAGACTCTCAGACAGAGTGGCTTTGATTAAC 1127
DB 721 GTTACATTAACCGGACATATATATAGAGACTCTCAGACAGAGTGGCTTTGATTAAC 780
QY 1128 GCCAAGCTTTTCCGGTATCCAGATCAACACTTGGCTTCAAAAATGAAACAATTT 1187
DB 781 GCCAAGCTTTTCCGGTATCCAGATCAACACTTGGCTTCAAAAATGAAACAATTT 840
QY 1188 ACCGACCGGCGGGTTTATATATCCCTCGGCTTATATGAAAGCTGATGTGCTC 1247
DB 841 ACCGACCGGCGGGTTTATATATCCCTCGGCTTATATGAAAGCTGATGTGCTC 900
QY 1248 AGTAGGCCATATCTTGGCTGATATCTGGCAGATGAACTCTTGGCAACCGTCTCC 1307

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Db 901 AGTAGCCCATATCTCTTGCTGATACCTGCGAGATGGAACCTCTTGGCAACCGCTTCCC 960
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 Db 961 GACTTCCTTAGAGAGGGAGCGCCACGAGAACTATTCGTGTAATTAAGTAATGCTGA 1020
 QY 1368 TTGTGTCATCAGATGCTTTTGGCGAAGAGAGATATAGGTTGGCACGACGCGCACT 1427
 Db 1021 TTGTGTCATCAGATGCTTTTGGCGAAGAGAGATATAGGTTGGCACGACGCGCACT 1080
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 QY 1488 GACGACTCGAAATCCACATATCAAAATATCCGAGTATGTAATAACCTCCAAACCGTGATG 1547
 Db 1141 GACGACTCGAAATCCACATATCAAAATATCCGAGTATGTAATAACCTCCAAACCGTGATG 1200
 QY 1548 GAATGGAACAACCTTTAAATCCGAGTATCCGAAATGATTTGATTTGCCAAATATAGATC 1607
 Db 1201 GAATGGAACAACCTTTAAATCCGAGTATCCGAAATGATTTGATTTGCCAAATATAGATC 1260
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 Db 1261 TCTGCGATGCGAGAAATCTCAGCGAGGAGTTCTATGAGGAGAGCGACACCTTTAGGCGAG 1320
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 Db 1381 TGGGACAAATCGATTCATTTAAACCGGAGAGTATGATGATGCGAACTGTATCAT 1440
 QY 1788 CGACTGAATCCCTGTAATCCGTTTGAATCCATATATAATTTTGGATGATTTGG 1847
 Db 1441 CGACTGAATCCCTGTAATCCGTTTGAATCCATATATAATTTTGGATGATTTGG 1500
 QY 1848 GAGCTTTTTCGACGTTCAAAATTTTTCGAACCCCTTTTGGAAACGAACCAACGCT 1907
 Db 1501 GAGCTTTTTCGACGTTCAAAATTTTTCGAACCCCTTTTGGAAACGAACCAACGCT 1560
 QY 1908 AGGCTGGAATGCCCATCTGTTGAGCAATTCACGTTCAATATAATGTCGTTCCGGGG 1967
 Db 1561 AGGCTGGAATGCCCATCTGTTGAGCAATTCACGTTCAATATAATGTCGTTCCGGGG 1620
 QY 1968 CGCAACTGCAACTCCGATATAATAACGCGCCCAACAACCGGCACTAAAGATGAAGAAGATT 2027
 Db 1621 CGCAACTGCAACTCCGATATAATAACGCGCCCAACAACCGGCACTAAAGATGAAGAAGATT 1680
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 Db 1861 TCCAGCGGTTCACTTTCCAGCGGATAGAAATGCGCGCGGCTTTCTTTATGTTTTGGC 1920
 QY 2268 GTCTTCATAGGACGTCGTTGGTGTATACGTTGGTTTTTTCTTTAGAGTTTAAAGATTGCT 2327
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 Db 2161 TGTACTCACCGTTCGCGAGACCACTATGAGCTCTCCCGGAGGGGGGAGTCTTGGAGGCTG 2220
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 Db 2221 CACGACCTCATATCTAAACCCATGCTTAAACGCTTTCTGCGTGAAGACAGTAGTTCTCA 2280
 QY 2628 CAGGGAGATATCATAGTGTGAGTGTCCGCCCATATAGGGGGGCTGGC 2674
 Db 2281 CAGGGAGATATCATAGTGTGAGTGTCCGCCCATATAGGGGGGCTGGC 2327

RESULT 5
 AAD27538/c
 ID AAD27538 standard; DNA; 5064 BP.
 XX
 AC AAD27538;
 XX
 DT 18-APR-2002 (first entry)
 DT
 XX
 DE pGL3 enhancer vector DNA.
 XX
 KW p53 protein; pGL3 luciferase reporter vector; luc+; transcription factor;
 KW cell cycle control; DNA damage repair; pGL3 enhancer vector; apoptosis;
 KW firefly; ds.
 XX
 OS Photinus pyralis.
 OS
 OS Unidentified.
 OS Chimeric.
 OS
 FH Key
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 FT complement(89..111)
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 FT 2005..2249
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 FT /note= "complement(2307..2326)"
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 FT /note= "Beta-lactamase gene"
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 FT 5006..5025
 FT /tag= k
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XX WO200196602-A2.
 XX 20-DEC-2001.
 XX 18-JUN-2001; 2001WO-GB002718.
 XX 16-JUN-2000; 2000GB-00014820.
 XX (MEDI-) MEDICAL RES COUNCIL.
 XX Yang AL, Feasting M;
 XX WPI; 2002-130743/17.
 XX
 XX Determining the p53 status of a sample, useful for assaying for mimetics
 XX or antagonists of p53, or for the presence of DNA damage, comprises
 XX determining whether p53 binds to the pGL3 vector in a sample containing a
 XX pGL3 vector.
 XX
 XX Claim 8; Page 39-42; 53pp; English.
 XX
 XX The patent discloses methods for determining the p53 status of a sample
 XX which comprise providing a sample containing a pGL3 luciferase reporter
 XX vector and determining whether p53 binds to the pGL3 vector. p53 is a
 XX transcription factor that regulates many genes including those associated
 XX with cell cycle control, apoptosis and DNA damage repair. pGL3 reporter
 XX vectors contain a modified firefly luciferase cDNA designated luc+. p53
 XX protein binds to pGL3-basic vector and causes luciferase expression. The
 XX method is useful for determining the p53 status of a sample. It is also
 XX useful for assaying for mimetics or antagonists of p53 and for assaying
 XX for presence of activated p53 and/or DNA damage. The invention also
 XX relates to a method of modifying pGL3 vector which involves deletion or
 XX alteration of a CCGGG motif of the pGL3 vector and/or deleting or
 XX altering a sequence within 20 bp sequence 5' or 3' of CCGGG motif. The
 XX nucleic acid having a sequence incorporating the CCGGG motif is useful
 XX for conferring promoter activity or p53-responsiveness on a nucleic acid
 XX encoding a polypeptide of interest or in assays for p53 transcriptional
 XX activity. The present DNA sequence is pGL3 enhancer vector sequence
 XX
 XX Sequence 5064 BP; 1300 A; 1201 C; 1242 G; 1321 T; 0 U; 0 Other;
 XX
 XX Query Match 63.6%; Score 1763.2; DB 6; Length 5064;
 XX Best Local Similarity 87.9%; Pred. No. 2.5e-227;
 XX Matches 2002; Conservative 0; Mismatches 168; Indels 108; Gaps 3;
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 XX 1 GGATCGCGTGGAAATGTGTGAGTGTAGAGTGTGAAAGTCCCGAGCTCCCGACAGCAG 60
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 XX |||||
 XX 61 CAGAAATATGCAAGAGCATCTCAATTAGTCAAGCAACAGGTGTGAAAGTCCCGACAG 120
 XX |||||
 XX 2199 CAGAAATATGCAAGAGCATCTCAATTAGTCAAGCAACAGGTGTGAAAGTCCCGACAG 2136
 XX |||||
 XX 121 CTCGCCAGAGGCAAGATATGCAAGAGCATCTCAATTAGTCAAGCAACCATATATCCC 180
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 XX 181 GCCCGTAATCGGCGCATCCGCGCTCAACTCCGCGCAGTCCGCGCATCTCCGCGCGCA 240
 XX |||||
 XX 2075 GCCCGTAATCGGCGCATCCGCGCTCAACTCCGCGCAGTCCGCGCATCTCCGCGCGCA 2016
 XX |||||
 XX 241 TGGCTGACTAATTTTTTTTATATATGCAAGGCGGAGCGCGCTCGAGCTATTT 300
 XX |||||
 XX 2015 TGG-----TTGAGATCTTATGATTT 1995
 XX |||||
 XX 301 CCGAAGATATGAGAGCGCTTTTGTAGAGCTTATGAGCTTTTGTAGAGCTTATGAGATC 360
 XX |||||
 XX 1994 TTACCAATTTTGTAGAGCTTTTACTTG----- 1968
 XX |||||
 XX 361 TGGAGAGAGGCGCATCTCTGTGAGTCAATGCGGCTCAGGAGCTTTTACAGAGCT 420
 XX |||||
 XX 1967 -----CTTTAAAAAACCTCCCAACCTTCCCTGAACTTAAACATATAATGAA 1919
 XX |||||

QY 421 AGCGTGACTAGGGCTAAGATGAGCCACATTAAGAAGAGAGAGAGAGAGAGAGAGAGAGAG 480
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 Db 1918 TGCATTTGTTGTTGTTAATTGTTATGACGCTTATTAATGTTACAAATTAAGCAATAG 1859
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 Db 1858 CATCAGAAATTTTCAAAATTAAGATTTTTCATCTGATCTGATGTTGTTGTTCCAA 1799
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 Db 1763 GCGCGCGCGCGCGCGCATCTTAAGATTAACAGGCGATCTTTCCGCGCTTCTGCGCTTTATG 1704
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 Db 1703 AGGATCTCTGATTTTCTTGGCGTGAATTTCCGTTAAGACCTTTGCGTTATGCTTC 1644
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 Db 1643 ACAAACAACACTCTCGCGCAACTTTTCCGCTTGTATCTGACCTGCGCACTTAATCC 1584
 QY 781 AGGATCTCTTTCCTGATGCTTTCCTGCTCAAAACAACAAGCGCGGAGAGT 840
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 Db 1523 TCACCGCGGTCATCTCGCGGAGAACCTCGACACCTCGCTGAGAGATTTGGGATGTTGG 1464
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 Db 1103 CTTGCTGATATCTGAGAGATGAACTCTTGGCAACGCTTCCCGACCTTCTTATAG 1044
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 Db 1043 AGGAGAGCGCCACAGAAAGCAATTTCTGTTAATTAATGATTAATGATTAATGATTA 984
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QY 1501 CCACATATCAAAATATCCGAGTGTAGTAAACATTCGAAAACCGTGTGATGGAATGGAACA 1560
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QY 1561 CTTAAATCCGAGTATCCGAAATGATTTGATTCGAAAATATAGATCTCTGCGCATGCGAG 1620
DB 803 CTTAAATCCGAGTATCCGAAATGATTTGATTCGAAAATATAGATCTCTGCGCATGCGAG 744
QY 1621 AATCTCAGCAGGAGATTCTATGAGGAGCAGACGACCTTTATGAGCAGACAGTATGATCA 1680
DB 743 AATCTCAGCAGGAGATTCTATGAGGAGCAGACGACCTTTATGAGCAGACAGTATGATCA 684
QY 1681 GAGAGTTCATGATCAGTACGAAATGTCTTGTCCCTATTCGAAAGACTCTGCGCAAAAATCG 1740
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QY 1921 CCCATACGTTGAGCAATTCACGTTCACTTAATAATGTGTTCCGCGGCGCAACTGCAACT 1980
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DB 323 ACGATTTCTGATTTGATTTCAAGCCCATATGCTTTCTATGCTTTCGCAACCGAACGAC 264
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DB 263 ATTTCGAAGTACAGCGGTAGTATGATCCACCGATGATGATGATGATTAAGCAAT 204
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DB 203 GTTTCAGGAACCAAGGCGATCTTCTCATAGCTTATGATGATGCTCTCCAGCGATTCCA 144
QY 2221 TCTTCAAGCGGATGATGAGCGCGCGCTTTCTTATGTTTTTGGCGTCTTCATG 2278
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RESULT 6

AAA07776/c

ID AAA07776 standard; DNA; 5256 BP.

AC AAA07776;

DT 03-JUL-2000 (first entry)

DE DNA sequence of plasmid pGL2.

XX ced-6; hliced-6; h2ced-6; signal transduction pathway; phagocytosis;
 KW cancer; autoimmune disease; neurodegenerative disease; stroke; AIDS;
 KW Huntington's disease; myocardial infarction; cytostatic; neuroprotective;
 KW cardiant; immunosuppressive; apoptosis modulator; luciferase; ss.

XX Synthetic.

OS WO964586-A2.

PN 16-DEC-1999.

```

XX 10-JUN-1999; 99WO-EP004043.
PF 11-JUN-1998; 98GB-00012660.
XX 24-SEP-1998; 98GB-00020816.
PR (DEVG-) DEYGEN NV.
XX Smits E, Van Cielinge WMR, Bogaert TAOE;
PI WPI; 2000-246285/21.
XX
XX Assays for determining the phagocytosis of apoptotic cells useful for
PT identifying a compound which influences the phagocytic uptake of
PT apoptotic cells and treats cancers and neurodegenerative diseases.
XX
XX Example; Fig 19; 122pp; English.
PS
XX The invention relates to assays involving two human homologues of
CC Caenorhabditis elegans ced-6 (hiced-6 and h2ced-6) for identifying
CC compounds which function as an inhibitor or an enhancer of a signal
CC transduction pathway. The assays are carried out by measuring
CC phagocytosis of apoptotic cells. The methods are useful for identifying
CC compounds which can act as apoptotic modulators which are useful for
CC treating diseases such as cancer, autoimmune diseases, neurodegenerative
CC diseases such as Huntington's disease, stroke, myocardial infarction and
CC AIDS. The assays are well adapted for medium and high throughput
CC screening using a multi-well plate format. The present sequence
CC represents the DNA sequence of plasmid pGL2 which is suitable for
CC introduction of reporter gene luciferase into Ba/K3 cells
XX
SQ Sequence 5256 BP; 1336 A; 1268 C; 1281 G; 1371 T; 0 U; 0 Other;

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Query Match 63.6%; Score 1763.2; DB 3; Length 5256;

Best Local Similarity 87.9%; Pred. No. 2.5e-227;

Matches 2002; Conservative 0; Mismatches 168; Indels 108; Gaps 3;

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QY 1 GGAATCCGCTGTGGAATGTGTGTCAGTTAGAGGTGGAAGTCCCGAGGCTCCCAAGAG 60
DB 2447 GGAATCCGCTGTGGAATGTGTGTCAGTTAGAGGTGGAAGTCCCGAGGCTCCCAAGAG 2388
QY 61 CAGAAGTATGCAAGAGCATCTCAATTAATGTCAGCAACAGGTGTGAAAGTCCCAAG 120
DB 2387 CAGAAGTATGCAAGAGCATCTCAATTAATGTCAGCAACAGGTGTGAAAGTCCCAAG 2328
QY 121 CTCGCCAGAGGAGAGAGTATGCAAGAGCATGATCTCAATTTAGTCAGCAACCATGATCCC 180
DB 2327 CTCGCCAGAGGAGAGAGTATGCAAGAGCATGATCTCAATTTAGTCAGCAACCATGATCCC 2268
QY 181 GCCCCTAATCTCGCCCATCCGCCCTAATCTCGGCCAATTCGCGCCATTCGCGCTCA 240
DB 2267 GCCCCTAATCTCGCCCATCCGCCCTAATCTCGGCCAATTCGCGCCATTCGCGCTCA 2208
QY 241 TGGCTGACTAATTTTTTATTTATATGACAGAGCGAGCGCGCTCGGCTCTGAGCTATT 300
DB 2207 TCG-----TTAGATTCCTTATGATTT 2187
QY 301 CCAGAAGTATGAGAGAGGCTTTTGGAGGCTTAGGCTTTTGCAAAAGCTTATGATC 360
DB 2186 TTACCAATTTGATGAGGTTTATCTTG----- 2160
QY 361 TGCAGAGAGGCGAGTATGACATCTCTGACGATCAATGGGCTCAGAGACCTTTCAAGCT 420
DB 2159 -----CTTAAAAAACTCCACACCTCCCTGAACTGAAACATTAATGAA 2111
QY 421 AGCGGTGACTAGAGGCTTAAGATGAGCCACATTAAGAAGAGAGAGAGAGAGAGAG 480
DB 2110 TGCATTTGTTGTTTAACTTTTATTTAGCAGCTTATATGTTTCAATTAAGCAATG 2051
QY 481 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 2050 CATCAGAAATTTCAAGAAATTAAGCATTTTTCATGCTGATCTTGTGTGTGTCCAA 1991

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| FT | enhancer | /note= "SV40 late poly(A) signal" |
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| FT | | /*tag= f |
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| FT | | /*tag= g |
| FT | misc_signal | /bound_moiety= "RV primer4" |
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| FT | misc_feature | /note= "ColEI-derived plasmid replication origin" |
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| FT | polyA_signal | /note= "R1 origin" |
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| FT | | /*tag= k |
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| XX | | |
| PN | WO200196602-A2. | |
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| PD | 20-DEC-2001. | |
| XX | | |
| PD | 18-JUN-2001; 2001WO-GB002718. | |
| XX | | |
| PR | 16-JUN-2000; 2000GB-00014820. | |
| XX | | |
| PA | (MED1-) MEDICAL RES COUNCIL. | |
| PI | Yang AL, Feasting M; | |
| XX | | |
| XX | WPI; 2002-130743/17. | |
| DR | | |
| XX | | |
| PT | Determining the p53 status of a sample, useful for assaying for mimetics | |
| PT | or antagonists of p53, or for the presence of DNA damage, comprises | |
| PT | determining whether p53 binds to the pGL3 vector in a sample containing a | |
| PT | pGL3 vector. | |
| XX | | |
| XX | Claim 20; Page 36-39; 53pp; English. | |
| PS | | |
| XX | | |
| XX | The patent discloses methods for determining the p53 status of a sample | |
| CC | which comprise providing a sample containing a pGL3 luciferase reporter | |
| CC | vector and determining whether p53 binds to the pGL3 vector. p53 is a | |
| CC | transcription factor that regulates many genes including those associated | |
| CC | with cell cycle control, apoptosis and DNA damage repair. pGL3 reporter | |
| CC | vectors contain a modified firefly luciferase cDNA designated luc+. p53 | |
| CC | protein binds to pGL3-basic vector and causes luciferase expression. The | |
| CC | method is useful for determining the p53 status of a sample. It is also | |
| CC | useful for assaying for mimetics or antagonists of p53 and for assaying | |
| CC | for presence of activated p53 and/or DNA damage. The invention also | |
| CC | relates to a method of modifying pGL3 vector which involves deletion or | |
| CC | alteration of a CCCGGG motif of the pGL3 vector and/or deleting or | |
| CC | altering a sequence within 20 bp sequence 5' or 3' of CCCGGG motif. The | |
| CC | nucleic acid having a sequence incorporating the CCCGGG motif is useful | |
| CC | for conferring promoter activity or p53-responsiveness on a nucleic acid | |
| CC | encoding a polypeptide of interest or in assays for p53 transcriptional | |
| CC | activity. The present DNA sequence is pGL3 control vector sequence | |
| XX | | |
| SQ | Sequence 5256 BP; 1336 A; 1268 C; 1281 G; 1371 T; 0 U; 0 Other; | |
| | Query Match 63.6%; Score 1763.2; DB 6; Length 5256; | |
| | Best Local Similarity 87.9%; Pred. No. 2.5e-227; | |
| | Matches 2002; Conservative 0; Mismatches 166; Indels 108; Gaps 3; | |
| 0Y | 1 GGATCCCGGTGGGAATGCTGTCACTTAAAGGCTGGGAAGTCCCAAGCTCCCAAGCAGG 60 | |
| 0b | 2447 GGATCCCGGTGGGAATGCTGTCACTTAAAGGCTGGGAAGTCCCAAGCTCCCAAGCAGG 2388 | |

| | | | |
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| QY | 61 | CAGAAAGTATGC | 120 |
| Db | 2387 | CAGAAAGTATGC | 2328 |
| QY | 181 | CTCCACGACGAG | 180 |
| Db | 2327 | CTCCACGACGAG | 2268 |
| QY | 181 | GCCCTTAAC | 240 |
| Db | 2267 | GCCCTTAAC | 2208 |
| QY | 241 | TGCGTGA | 300 |
| Db | 2207 | TGCGTGA | 2187 |
| QY | 301 | CCAGAAAGTATGC | 360 |
| Db | 2186 | TTACACATTTGTATG | 2160 |
| QY | 381 | TGCAGAGGCGCAG | 420 |
| Db | 2159 | CTTTAAAAA | 2111 |
| QY | 421 | AGCCGTGACTAG | 480 |
| Db | 2110 | TGCAATGTGTGT | 2051 |
| QY | 481 | AGAAAGAAAG | 540 |
| Db | 2050 | CATCAAAATTTCA | 1991 |
| QY | 541 | AAAAA | 600 |
| Db | 1990 | ACTCATCATGTAT | 1956 |
| QY | 601 | GCCGGAAGT | 660 |
| Db | 1955 | GCGCGCGCGCG | 1896 |
| QY | 661 | AGGATCTCTG | 720 |
| Db | 1895 | AGGATCTCTG | 1836 |
| QY | 721 | ACAAACA | 780 |
| Db | 1835 | ACAAACA | 1776 |
| QY | 781 | ACGATCTCT | 840 |
| Db | 1775 | ACGATCTCT | 1716 |
| QY | 841 | TCACCGCGCAT | 900 |
| Db | 1715 | TCACCGCGCAT | 1656 |
| QY | 901 | AGCAAGATG | 960 |
| Db | 1655 | AGCAAGATG | 1596 |
| QY | 961 | TTGAGGCGGT | 1020 |
| Db | 1595 | TTGAGGCGGT | 1436 |
| QY | 1021 | TGTAGCATCAT | 1080 |
| Db | 1535 | TGTAGCATCAT | 1476 |
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| Db | 1475 | GACATTAATCA | 1416 |


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QY 1141 CCGGATCCAGATCCAACTTCCTGCTTCAAAAAATGAGAACACTTACCGACCGGCC 1200
|
|
|
Db 1415 CCGGATCCAGATCCAACTTCCTGCTTCAAAAAATGAGAACACTTACCGACCGGCC 1356
|
|
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QY 1201 GGTATATATATATATATATATATATATATATATATATATATATATATATATAT 1260
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Db 1355 GGTATATATATATATATATATATATATATATATATATATATATATATATATAT 1296
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|
QY 1261 CCTTGCTGATATATATATATATATATATATATATATATATATATATATATATAT 1320
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|
|
Db 1295 CCTTGCTGATATATATATATATATATATATATATATATATATATATATATATAT 1236
|
|
|
QY 1321 AGGGAGCGCCACCAAGAACATTTGTGTAAATATATATATATATATATATATATAT 1380
|
|
|
Db 1235 AGGGAGCGCCACCAAGAACATTTGTGTAAATATATATATATATATATATATATAT 1176
|
|
|
QY 1381 GTGCTTTTGGCGAAGAGAGAAATAGAGTTGGCAGCAGCAGCAGCAGCAGCAGCAG 1440
|
|
|
Db 1175 GTGCTTTTGGCGAAGAGAGAAATAGAGTTGGCAGCAGCAGCAGCAGCAGCAGCAG 1116
|
|
|
QY 1441 TCTGAAAGGCTCTCGAAGAACAGCTCTTCTTCAAACTTATATATATATATATAT 1500
|
|
|
Db 1115 TCTGAAAGGCTCTCGAAGAACAGCTCTTCTTCAAACTTATATATATATATATAT 1056
|
|
|
QY 1501 CCACATATCAAAATATCGAGTATATATATATATATATATATATATATATATATAT 1560
|
|
|
Db 1055 CCACATATCAAAATATCGAGTATATATATATATATATATATATATATATATATAT 996
|
|
|
QY 1561 CTTAAATATCGAGTATCGGAAATATATATATATATATATATATATATATATATAT 1620
|
|
|
Db 995 CTTAAATATCGAGTATCGGAAATATATATATATATATATATATATATATATATAT 936
|
|
|
QY 1621 AATCTACCGAGGCAATTTATATAGAGCAAGCAGCAGCAGCAGCAGCAGCAGCAG 1680
|
|
|
Db 935 AATCTACCGAGGCAATTTATATAGAGCAAGCAGCAGCAGCAGCAGCAGCAGCAG 876
|
|
|
QY 1681 GAGGATTCATGATCGATGCAATTTCTTGTCTTCTTCAAACTTATATATATATATAT 1740
|
|
|
Db 875 GAGGATTCATGATCGATGCAATTTCTTGTCTTCTTCAAACTTATATATATATATAT 816
|
|
|
QY 1741 TATTCATTAACCCGGAGGATGATGATGATGATGATGATGATGATGATGATGATG 1800
|
|
|
Db 815 TATTCATTAACCCGGAGGATGATGATGATGATGATGATGATGATGATGATGATG 756
|
|
|
QY 1801 TGGTAATCCGTTTATATATATATATATATATATATATATATATATATATATATAT 1860
|
|
|
Db 755 TGGTAATCCGTTTATATATATATATATATATATATATATATATATATATATATAT 696
|
|
|
QY 1861 AGGTCAAAATTTTGGCAACCCCTTTTGGAAAGCAACCCGAGTATGAGGCTGCGAATG 1920
|
|
|
Db 695 AGGTCAAAATTTTGGCAACCCCTTTTGGAAAGCAACCCGAGTATGAGGCTGCGAATG 636
|
|
|
QY 1921 CCCATCTGTTGAGCAATTCAGCTTATATATATATATATATATATATATATATATATAT 1980
|
|
|
Db 635 CCCATCTGTTGAGCAATTCAGCTTATATATATATATATATATATATATATATATATAT 576
|
|
|
QY 1981 CCGATTAATTAACCGCCCAACCCGAGTATGAGGCTGCGAATGAGAGGTTTTCATGCA 2040
|
|
|
Db 575 CCGATTAATTAACCGCCCAACCCGAGTATGAGGCTGCGAATGAGAGGTTTTCATGCA 516
|
|
|
QY 2041 AGGATCTGATGATTTATATATATATATATATATATATATATATATATATATATAT 2100
|
|
|
Db 515 AGGATCTGATGATTTATATATATATATATATATATATATATATATATATATATATAT 456
|
|
|
QY 2101 ATTTCAAGTATCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2160
|
|
|
Db 455 ATTTCAAGTATCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 396
|
|
|
QY 2161 GTTTCAGAGAACCGGGGATATCTTCTTATATATATATATATATATATATATATATAT 2220
|
|
|
Db 395 GTTTCAGAGAACCGGGGATATCTTCTTATATATATATATATATATATATATATATAT 336
|
|
|
QY 2221 TCTTCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2278

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Db 335 TCTTCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 278
|
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RESULT 8
ADN11354/C
ID ADN11354 standard; DNA; 7014 BP.
XX
XX
AC ADN11354;
PT
DT 15-JUL-2004 (first entry)
XX
DE GAGGS-Fluc nucleotide sequence SEQ ID NO:15.
XX
XX expression vector; short hairpin RNA; shRNA;
XX constitutive gene knock down; inducible gene knock down;
XX polymerase II dependent locus; gene therapy; gene; ds.
XX Synthetic.
XX
XX MO2004035782-A2.
XX
XX 29-APR-2004.
XX
XX 10-OCT-2003; 2003WO-BP011233.
XX
XX 17-OCT-2002; 2002EP-00023283.
XX
XX 02-MAY-2003; 2003US-0467814P.
XX
XX 10-JUL-2003; 2003US-0485969P.
XX
XX (ARTE-) ARTEMIS PHARM GMBH.
XX
PI Seibler J, Schwenk F, Kuehn R, Kueter-Luks B;
XX
XX WPI; 2004-348459/32.
XX
XX
XX New expression vector comprising a short hairpin RNA (shRNA) construct
XX under the control of a ubiquitous promoter, useful for constitutive
XX and/or inducible gene knock down in a vertebrate, or in a tissue.
XX
XX
XX Example 3; SEQ ID NO 15; 70bp; English.
XX
XX
XX The present invention describes an expression vector comprising a short
XX hairpin RNA (shRNA) construct under the control of a ubiquitous promoter.
XX Also described: (1) a method for constitutive and/or inducible gene knock
XX down in a vertebrate, or in a tissue culture or cells of a cell culture
XX derived from a vertebrate by stably integrating an expression vector into
XX the genome of the vertebrate, of the tissue culture or of the cells of
XX the cell culture; and (2) a vertebrate or tissue or cell culture derived
XX from a vertebrate having stably integrated, preferably at a polymerase II
XX dependent locus or the vertebrate, tissue culture or cells of the tissue
XX culture, an expression vector as defined above. The expression vector can
XX be used in gene therapy. The expression vector is useful for preparing an
XX agent, shRNA, for constitutive and/or inducible gene knock down in a
XX vertebrate, or in a tissue culture or cells of a cell culture derived
XX from a vertebrate. The present sequence represents a nucleotide sequence
XX which is used in the exemplification of the present invention.
XX
XX
XX Sequence 7014 BP; 1588 A; 1756 C; 1953 G; 1717 T; 0 U; 0 Other;
XX
XX
XX Query Match 63.6%; Score 1763.2; DB 12; Length 7014;
XX Best Local Similarity 87.9%; Pred. No. 2.4e-227;
XX Matches 2002; Conservative 0; Mismatches 168; Indels 108; Gaps 3;
XX
QY 1 GGATCGCTGTGGAATGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 60
|
|
|
Db 4183 GGATCGCTGTGGAATGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 4124
|
|
|
QY 61 CAGAATGATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
|
|
|
Db 4123 CAGAATGATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 4064
|
|
|
QY 121 CTCGCCAGCAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 180

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Db 4063 CCCCCAGCAGGAGCAAGTATGCAAAAGCATCATCTCAATTAGTCAGAACCATATAGTCCC 4004
Qy 181 GGCCTTAATCTCGGCGCAATCCGGCCCTPAATCCGCCCAAGTTCCGCCCAATTTCCGCCCA 240
Db 4003 GCCCTTAATCTCGGCGCAATCCGGCCCTPAATCCGCCCAAGTTCCGCCCAATTTCCGCCCA 3944
Qy 241 TGGCTGAATTAATTTTATTTATTTATGAGAGCGGCGGCTCGGCTCTGAGCTATT 300
Db 3943 TCG-----TTCAAGTCTTTATTCGATT 3923
Qy 301 CCAGAAATGATGAGAGGCTTTTGTGAGGCTTAGGCTTTTGGCAAAAAGCTTACATGATC 360
Db 3922 TTACCAATTTGTAGAGTTTACTTG----- 3896
Qy 361 TGCAGAGGCGCAGTATCAGCACTCTCGCAGATGCGGCTCAGGACCTTTACAGCT 420
Db 3895 -----CTTTAAAAAAGCTTCCACACCTCCCTGAACTGTAACCTGAAACATAAATGAA 3847
Qy 421 AGCGGTGATAGGGCTAGATGAGAGCACTTAAGAAGAGAAAGAAAGAAAGAA 480
Db 3846 TGCATTTGTTGTGTTAACTTTTATTTGAGCTTATATGTTACAAATTAAGCAATAG 3787
Qy 481 AGAAGGAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 540
Db 3786 CATCACAAATTTCAAAATTAAGCATTTTTCATGCTATCTAGTTGTGTTGTCMA 3727
Qy 541 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAATGCTTAAGA 600
Db 3726 ACTCATCAATGTATCTTATCA-----TGTCTGCTCGAAGC 3692
Qy 601 GCGCGAGTGTTTAACCCCAACTTTAAACGGCGATCTTTCGCGCTTCTTGACCTTATG 660
Db 3691 GCGCGCGCGCGCGCACTAGAAATTAACGGCGATCTTTCGCGCTTCTTGACCTTATG 3692
Qy 661 AGGATCTCTGATTTTCTTGCGTGAATTTTCGGTAAAGACTTTTCGGTACTTGCTTC 720
Db 3631 AGGATCTCTGATTTTCTTGCGTGAATTTTCGGTAAAGACTTTTCGGTACTTGCTTC 3572
Qy 721 ACAACACAACTCTCGCGCGCACTTTTCGGCGTGTACTTGAACGGGAGCATATCC 780
Db 3571 ACAACACAACTCTCGCGCGCACTTTTCGGCGTGTACTTGAACGGGAGCATATCC 3512
Qy 781 ACGATCTCTTTTCCGTCATGTCCTTTCGCTGCTCAAAAACAACAGCGCGCGGAAAT 840
Db 3511 ACGATCTCTTTTCCGTCATGTCCTTTCGCTGCTCAAAAACAACAGCGCGCGGAAAT 3452
Qy 841 TCACCGGCGTCATGTCGGGAAAGACTGCGACACCTGCGTGAAGATGTTGGGCTGTGG 900
Db 3451 TCACCGGCGTCATGTCGGGAAAGACTGCGACACCTGCGTGAAGATGTTGGGCTGTGG 3392
Qy 901 AGCAAGATGATTCOAATTCAGGGGAGCGACCTGATAGGCTTTGTATTAATCAAGAG 960
Db 3391 AGCAAGATGATTCOAATTCAGGGGAGCGACCTGATAGGCTTTGTATTAATCAAGAG 3332
Qy 961 TTCAGGCGGTCAACGATGAAGAGTTCCTTCCGTCAGTAAAGTATGTCTCCAGAA 1020
Db 3331 TTCAGGCGGTCAACGATGAAGAGTTCCTTCCGTCAGTAAAGTATGTCTCCAGAA 3272
Qy 1021 TGTAGCCATCAATCTTTGATCAATCAAGGCGTGTGCTTCGGATTTGTATCAATAACG 1080
Db 3271 TGTAGCCATCAATCTTTGATCAATCAAGGCGTGTGCTTCGGATTTGTATCAATAACG 3212
Qy 1081 GACATATCATAGGAACTCTCAACAAGTTGCGCTTTGATTAACGCCCAAGCTTTTC 1140
Db 3211 GACATATCATAGGAACTCTCAACAAGTTGCGCTTTGATTAACGCCCAAGCTTTTC 3152
Qy 1141 CCGGATATCAGATCAACAACCTTCGCTTCAAAAATGAAACAATTTTCCGACCGGCGC 1200
Db 3151 CCGGATATCAGATCAACAACCTTCGCTTCAAAAATGAAACAATTTTCCGACCGGCGC 3092
Qy 1201 GGTTTATCATCCCTCGGCTGTAATCAGAAATGCTGATGTACTTCAAGTGAAGCCATAT 1260
Db 3091 GGTTTATCATCCCTCGGCTGTAATCAGAAATGCTGATGTACTTCAAGTGAAGCCATAT 3032
Qy 1261 CTTGCTGATTAATCTGGCAATAGAACTTTTGGCAACCGCTTCCCGGACTTCTTATAG 1320
Db 3031 CTTGCTGATTAATCTGGCAATAGAACTTTTGGCAACCGCTTCCCGGACTTCTTATAG 2972
Qy 1321 AGGGAGCGCGCACAGAAAGCAATTTGTGTAATTTAGATTAATCGTATTTGTCAATCAGA 1380
Db 2971 AGGGAGCGCGCACAGAAAGCAATTTGTGTAATTTAGATTAATCGTATTTGTCAATCAGA 2912
Qy 1381 GTGCTTTTGGCGAAGAGAGAAATAGGGTTGGCAGCAGCGCACTTTGAATCTTGTAA 1440
Db 2911 GTGCTTTTGGCGAAGAGAGAAATAGGGTTGGCAGCAGCGCACTTTGAATCTTGTAA 2852
Qy 1441 TCCGAAAGGCTCTCGAAGAACAGCTCTTCTTAATCTTATCAATTAAGCAATCGAAAT 1500
Db 2851 TCCGAAAGGCTCTCGAAGAACAGCTCTTCTTAATCTTATCAATTAAGCAATCGAAAT 2792
Qy 1501 CCACATATCAATATCCAGTGTAGTAAACATTCACAAAACCGTATGAAATGAAACA 1560
Db 2791 CCACATATCAATATCCAGTGTAGTAAACATTCACAAAACCGTATGAAATGAAACA 2732
Qy 1561 CTTAAATCGCAGTATCCGGAATGATTTGATTCGCAAAAATAGGATCTTGCGATCGAG 1620
Db 2731 CTTAAATCGCAGTATCCGGAATGATTTGATTCGCAAAAATAGGATCTTGCGATCGAG 2672
Qy 1621 AATCTACGAGGCACTTCTATAGGCAAGGCAACCTTTAGCGAGACCAATGATCCA 1680
Db 2671 AATCTACGAGGCACTTCTATAGGCAAGGCAACCTTTAGCGAGACCAATGATCCA 2612
Qy 1681 GAGAGTTCATGATCACTGCAATTTCTTGCTCCCTATCGAAGGACTCTGCACAAAATCG 1740
Db 2611 GAGAGTTCATGATCACTGCAATTTCTTGCTCCCTATCGAAGGACTCTGCACAAAATCG 2552
Qy 1741 TATTCATTAACCGGAGAGTATGATGTCAGCAAGCTGTACATGCACTGAATCCC 1800
Db 2551 TATTCATTAACCGGAGAGTATGATGTCAGCAAGCTGTACATGCACTGAATCCC 2492
Qy 1801 TGGTAATCCGTTTAAATCCAGTAATATTTTGTGATGATTTGGAGCTTTTTCG 1860
Db 2491 TGGTAATCCGTTTAAATCCAGTAATATTTTGTGATGATTTGGAGCTTTTTCG 2432
Qy 1861 ACGTTCAAAATTTTTCGAACCCCTTTTGGAAACGAACAACGATAGGCTGCAAAATG 1920
Db 2431 ACGTTCAAAATTTTTCGAACCCCTTTTGGAAACGAACAACGATAGGCTGCAAAATG 2372
Qy 1921 CCCATCTGTGAGCAATTCAGTTCATTAATATGTCGCGGCGCAACTGCACT 1980
Db 2371 CCCATCTGTGTAGCAATTCAGTTCATTAATATGTCGTCGCGGCGCAACTGCACT 2312
Qy 1981 CCGATTAATTAACCGCGCCAAACCGGCAATTAAGATTTGAAGAGTTTCACTGCAATAG 2040
Db 2311 CCGATTAATTAACCGCGCCAAACCGGCAATTAAGATTTGAAGAGTTTCACTGCAATAG 2252
Qy 2041 ACGATCTGTGATTTGTATTCAGCCCATATCGTTTCATATGCTTTCGCAACGAAACGAG 2100
Db 2251 ACGATCTGTGATTTGTATTCAGCCCATATCGTTTCATATGCTTTCGCAACGAAACGAG 2192
Qy 2101 ATTTGAACTACTCAGCGTAAATGATGTCACCTGATATGTCATCTGTAAAGCAATT 2160
Db 2191 ATTTGAACTACTCAGCGTAAATGATGTCACCTGATATGTCATCTGTAAAGCAATT 2132
Qy 2161 GTTTCAGGAACCAAGGCGGTATCTTTCATAGCTTATAGAGTTGCTTCAGCGTTCCA 2220
Db 2131 GTTTCAGGAACCAAGGCGGTATCTTTCATAGCTTATAGAGTTGCTTCAGCGTTCCA 2072
Qy 2221 TCTTCCAGGGAATAGAAATGCGCGCGCTTCTTTATGTTTGGCGTCCATAGG 2278
Db 2071 TCTTCCAGGGAATAGAAATGCGCGCGCTTCTTTATGTTTGGCGTCCATAGG 2014
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RESULT 9
AAD31131

| | |
|----------------------------|---|
| ID | AADJ1131 standard; DNA; 7788 BP. |
| XX | |
| XX | AADJ1131; |
| XX | |
| DT | 21-AUG-2002 (first entry) |
| XX | |
| XX | pCFUSII plasmid. |
| XX | |
| KM | Reporter construct; transcription control element; cell surface receptor; G-protein coupled receptor; GPCR; tyrosine kinase-type receptor; ion channel; high-throughput screening; HTS; jelly fish; EGFP; |
| KW | enhanced green fluorescent protein; TRB; TPA responsive element; |
| KM | 12-O-tetradecanoylphorbol-13-acetate; CWM; promoter; firefly; luciferase; |
| XX | sibian virus 40; SV40; pCFUSII plasmid; chimeric; ds. |
| XX | |
| OS | Cytomegalovirus. |
| OS | Aequorea victoria. |
| OS | Photinus pyralis. |
| OS | Rhesus macaque polyoma virus. |
| OS | Synthetic. |
| XX | Chimeric. |
| PM | WO200220749-A2. |
| XX | |
| PD | 14-MAR-2002. |
| PF | 06-SEP-2001; 2001WO-IB001938. |
| PR | 07-SEP-2000; 2000US-0230705P. |
| PA | (OMMA/) OMMAN C S O. (OLDE/) OLDE B A. (KOTA/) KOTARSKY K. |
| PI | Ozman SO, Olde BA, Kotarsky K; |
| XX | |
| XX | WPI; 2002-415727/44. |
| PT | |
| PT | Reporter construct with a chimeric reporter gene linked to transcription control element(s), useful for detecting substances that interact with cell surface receptors, e.g. G-protein coupled receptor family or ion channels. |
| PT | |
| PS | Example 2; Page 59-62; 66pp; English. |
| XX | |
| CC | The invention relates to a reporter construct, comprising a chimeric reporter gene (comprising coding sequences from two different genes fused to produce a gene product that is detectable without the need to lyse or otherwise destroy or diminish the viability of the cell in which they are expressed) operably linked to at least one transcription control element. The reporter construct is useful for detecting substances that interact with cell surface receptors, such as those of the G-protein coupled receptor family, tyrosine kinase-type receptors or ion channels. The construct is particularly useful in high-throughput screening assays. The construct is used in recombinant G-protein coupled receptor assays which are more sensitive and less labour and time-intensive than previous assays. The present sequence is pCFUSII plasmid comprising TPA (12-O- tetradecanoylphorbol-13-acetate) responsive elements (TRRE), minimal Cytomegalovirus promoter, Aequorea victoria enhanced green fluorescent protein (EGFP) gene, firefly luciferase gene, sibian virus 40 (SV40) promoter and neomycin resistance cassette |
| SO | Sequence 7788 BP; 1777 A; 2051 C; 1970 G; 1990 T; 0 U; 0 Other; |
| Query Match | 63.5%; Score 1758.2; DB 6; Length 7788; |
| Best Local Similarity | 87.9%; Pred. No. 1.1e-226; |
| Matches 1997; Conservative | 0; Mismatches 168; Indels 108; Gaps 3 |
| 0Y | 6 GCCTGGCAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCACAGGCTCCCGAGAGGCAGA 65 |
| Ddb | 13 CCCTGTGAATGTGTGTCAATTAGGGTGTGGAAAGTCCCCAAGGCTCCCGAGAGGCAGA 72 |
| 0Y | 66 GTATCCAAGCATCTCATTTGATGTCAGCAACGAGTGTTGGAAGTCCCGAGGCTGCC 125 |

Db 1045 ATCCAGATCCACAACCTTCGCTTCAAAAAATGGAACAATTACGACCGCCCGGCTT 1104
Qy 1206 ATCATCCCCCTGGGTGTATTCAGAAATAGCTAGTGTCTGATGAGCCCATCTCTG 1265
Db 1105 ATATCCCCCTGGGTGTATTCAGAAATAGCTAGTGTCTGATGAGCCCATATCTTGG 1164
Qy 1266 CTTGATACCTGGGAGATGGAACCTCTTGGCAACCGCTTCCCGACTTCTTAGAGAGGG 1325
Db 1165 CTTGATACCTGGGAGATGGAACCTCTTGGCAACCGCTTCCCGACTTCTTAGAGAGGG 1224
Qy 1326 AGCGCCACCGAAGCAATTTCTGTATTAATAGTAAATGCTATTTGTCAATCAGATGCT 1385
Db 1225 AGCGCCACCGAAGCAATTTCTGTATTAATAGTAAATGCTATTTGTCAATCAGATGCT 1284
Qy 1386 TTGGGAGAGAGAGATAGGGGTGGCAGCAGCAGGCACTTTGATCTTGTATCTCTG 1445
Db 1285 TTGGGAGAGAGAGATAGGGGTGGCAGCAGCAGGCACTTTGATCTTGTATCTCTG 1344
Qy 1446 AAGGCTCTTGAGAACAGCTCTTCTCAATCTATACATTAGACGACTTGAAATCCACA 1505
Db 1345 AAGGCTCTTGAGAACAGCTCTTCTCAATCTATACATTAGACGACTTGAAATCCACA 1404
Qy 1506 TATCAATATCCGAGCTGTAGTAAACATTCGAAACCGTGTATGAAATGAAACACCTTAA 1565
Db 1405 TATCAATATCCGAGCTGTAGTAAACATTCGAAACCGTGTATGAAATGAAACACCTTAA 1464
Qy 1566 AATCGAGATCCGGAATGATTTGATTGCAAAATAGATCTCTGAGCATGCGAGATCT 1625
Db 1465 AATCGAGATCCGGAATGATTTGATTGCAAAATAGATCTCTGAGCATGCGAGATCT 1524
Qy 1626 CACGACAGGAGTTCTATGAGGCAAGGCAACCTTTAGGCAACAGTATGATCAGAGGA 1685
Db 1525 CACGACAGGAGTTCTATGAGGCAAGGCAACCTTTAGGCAACAGTATGATCAGAGGA 1584
Qy 1686 GTTCATGATAGTGCATTTCTTGTCCCTATGGAAGGATCTGCGACAAATCGTATTC 1745
Db 1585 GTTCATGATAGTGCATTTCTTGTCCCTATGGAAGGATCTGCGACAAATCGTATTC 1644
Qy 1746 ATTAACACGGGAGATGATGATGATGACGAAGTGTATCATGATGATCCCTGGTA 1805
Db 1645 ATTAACACGGGAGATGATGATGATGACGAAGTGTATCATGATGATCCCTGGTA 1704
Qy 1806 ATCCGTTTGAATTCATGATTAATTTTGTGATGATTTGGAGCTTTTGTGACGTT 1865
Db 1705 ATCCGTTTGAATTCATGATTAATTTTGTGATGATTTGGAGCTTTTGTGACGTT 1764
Qy 1866 CAAAATTTTGAACCCCTTTTGGAAACGAACACCGATAGGCTGCGAAATGCCAT 1925
Db 1765 CAAAATTTTGAACCCCTTTTGGAAACGAACACCGATAGGCTGCGAAATGCCAT 1824
Qy 1926 ACTGTTGAGCAATTCAGTTCAATTATATGTCGTCGCGGCGCAACTGCACTCCGAT 1985
Db 1825 ACTGTTGAGCAATTCAGTTCAATTATATGTCGTCGCGGCGCAACTGCACTCCGAT 1884
Qy 1986 AATTAACGCGCCCAACACCGGCAATTAAGAAATGAAGAGATTTTCACTGCATACGAGAT 2045
Db 1885 AATTAACGCGCCCAACACCGGCAATTAAGAAATGAAGAGATTTTCACTGCATACGAGAT 1944
Qy 2046 TCTGTGATTTGTATTCAGCCCATATGTTTCATAGTCTTGCACACCGAAGCAATTTTC 2105
Db 1945 TCTGTGATTTGTATTCAGCCCATATGTTTCATAGTCTTGCACACCGAAGCAATTTTC 2004
Qy 2106 GAGTACTCAGCGTAAGTATGTCACCTCGATATGTCATCTGTAAAGCAATTTGTTCC 2165
Db 2005 GAGTACTCAGCGTAAGTATGTCACCTCGATATGTCATCTGTAAAGCAATTTGTTCC 2064
Qy 2166 AGGAACCGAGGCGTATCTTTCATAGCCTTATGCACTTCTCAGCGGTTCCATCTTC 2225
Db 2065 AGGAACCGAGGCGTATCTTTCATAGCCTTATGCACTTCTCAGCGGTTCCATCTTC 2124
Qy 2226 CAGCGATAGAAATGGCGCGCGGCTTTCTTATAGTTTGGGCTCTTCCATGCG 2278
Db 2125 CAGCGATAGAAATGGCGCGCGGCTTTCTTATAGTTTGGGCTCTTCCATGCG 2177

RESULT 10
AAD31132
ID AAD31132 standard; DNA; 7312 BP.
XX
AC AAD31132;
XX
DT 21-AUG-2002 (first entry)
XX
DE pCFUSII-IE plasmid.
XX
KW Reporter construct; transcription control element; cell surface receptor;
KW G-protein coupled receptor; GPCR; tyrosine kinase-type receptor;
KW ion channel; high-throughput screening; HTS; jelly fish; EGFP;
KW enhanced green fluorescent protein; TRF; TPA responsive element;
KW 12-O-tetradecanoylphorbol-13-acetate; GMV; promoter; firefly; luciferase;
KW pCFUSII-IE plasmid; chimeric; ds.
XX
OS Cyomegalovirus.
OS Aequorea victoria.
OS Photinus pyralis.
OS unidentified baculovirus.
OS Synthetic.
OS Chimeric.
XX
PN MO200220749-A2.
XX
PD 14-MAR-2002.
XX
PF 06-SEP-2001; 2001WO-1B001936.
XX
PR 07-SEP-2000; 2000US-0230705P.
XX
PA (OMNA/) OMNAN C S O.
PA (OLDE/) OLDE B A.
PA (KOTR/) KOTARSKY K.
XX
PI Ommann CSO, Olde BA, Kotarsky K;
XX
DR MPI, 2002-415727/44.
XX
PT Reporter construct with a chimeric reporter gene linked to transcription
PT control element(s), useful for detecting substances that interact with
PT cell surface receptors, e.g. G-protein coupled receptor family or ion
PT channels.
XX
PS Example 6; Page 62-64; 66pp; English.
XX
CS The invention relates to a reporter construct, comprising a chimeric
CC reporter gene (comprising coding sequences from two different genes fused
CC to produce a gene product that is detectable without the need to lyse or
CC otherwise destroy or diminish the viability of the cell in which they are
CC expressed) operably linked to at least one transcription control element.
CC The reporter construct is useful for detecting substances that interact
CC with cell surface receptors, such as those of the G-protein coupled
CC receptor family, tyrosine kinase-type receptors or ion channels. The
CC construct is particularly useful in high-throughput screening assays. The
CC construct is used in recombinant G-protein coupled receptor assays which
CC are more sensitive and less labour and time-intensive than previous
CC assays. The present sequence is pCFUSII-IE plasmid comprising TPA (12-O-
CC tetradecanoylphorbol-13-acetate) responsive elements (TREs), minimal
CC Cyomegalovirus promoter, Aequorea victoria enhanced green fluorescent
CC protein (EGFP) gene, firefly luciferase gene, baculovirus promoter and
CC neomycin resistance cassette
XX
SQ Sequence 7312 BP; 1702 A; 1889 C; 1836 G; 1885 T; 0 U; 0 Other;
XX
Query Match 63.1%; Score 1747.2; DB 6; Length 7312;
Best Local Similarity 87.8%; Pred. No. 3.3e-225;
Matches 1997; Conservative 0; Mismatches 168; Indels 109; Gaps 4;
Qy 6 CGCTGTGAAATGTTGTACATTAGAGTGTGAAAGTCCCAAGCTCCCAAGACGACGACGAA 65

| | | | |
|----|------|---|------|
| Db | 13 | CGCTGGAAATGTGTGATGATTAGGGTGTGAAAAGTCCCAAGGCTCCCAACAGACGAA | 72 |
| Oy | 66 | GTATGCAAAAGATGCATCTCAATTAGTCAGAGAAACAAGGTGTGAAAAGTCCCAAGGCTCC | 125 |
| Db | 73 | GTATGCAAAAGATGCATCTCAATTAGTCAGAGAACCAAGGTGTGAAAAGTCCCAAGGCTCC | 132 |
| Oy | 126 | CAGCAGGAGAAAGTATGCAAAAGCATGATCTCAATTAGTCAGAACCAATAGTCCGCCCC | 185 |
| Db | 133 | CAGCAGGAGAAAGTATGCAAAAGCATGATCTCAATTAGTCAGAACCAATAGTCCGCCCC | 192 |
| Oy | 186 | TAACTCCGCCCATCCCGCCCCCTAACTCCGCCCAAGTCCGCCCATTTCTCCGCCCATAGCT | 245 |
| Db | 193 | TAACTCCGCCCATCCCGCCCCCTAACTCCGCCCAAGTCCGCCCATTTCTCCGCCCATAGC-- | 250 |
| Oy | 246 | GACTAATTTTTTTTATTTATATGCAAGAGCGGAGCGCGCTCGAGCCCTAGGATTTTCAGA | 305 |
| Db | 251 | -----TTCAAGATCTTATATGATTTTATCC | 273 |
| Oy | 306 | AGTAGTAGAGAGCTTTTTTGTGAGGCGCTTAGGCTTTTGCAAAAAGCTTACATGATCTGCA | 365 |
| Db | 274 | ACATTTGTAGAGGTTTACTTG----- | 295 |
| Oy | 366 | AGAGGCCAGTATCAGCACTCTCTGCAATGCGGCTACGGACCTTTCACAGCTAGCCG | 425 |
| Db | 296 | -----CTTTAAAAAACTCCACACCTCCCTCGAAGCTGAAAATATAATGATGATGAA | 349 |
| Oy | 426 | TGACTAGGGCTTAAGTGAAGCACCATTAAGAAAGAGAAAGAAAGAAAGAAAGAAAG | 485 |
| Db | 350 | TTGTGTGTTTAACTGTTTATGTGACGTTTAAATAGTTTACAAATTAAGCAATGATCA | 409 |
| Oy | 486 | GAAGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA | 545 |
| Db | 410 | CAAAATTCACAAATTAAGCATTTTTTTCACATGCAATTCATAGTTGTGTGTTGTCAAACCTCA | 469 |
| Oy | 546 | AA | 605 |
| Db | 470 | TCAATGTATCTTATCA-----TGCTGCTCGAAGCGGCG | 504 |
| Oy | 606 | GAGAGTTTAAACCCAACTTTAAAGGAGATCTTTCCGCGCTTCTTGCGCTTATAGAGAT | 665 |
| Db | 505 | GCGCGCCGACTGTAGAAATACACGGGCATCTTTCCGCTTCTTGCGCTTATAGAGAT | 564 |
| Oy | 666 | CTCTGTGATTTTCTTGCGTGAAGTTTCCGGTAAAGACCTTCCGGTACTTGTGTCACAAA | 725 |
| Db | 565 | CTCTGTGATTTTCTTGCGTGAAGTTTCCGGTAAAGACCTTCCGGTACTTGTGTCACAAA | 624 |
| Oy | 726 | CACAACTCTCCGCGCAACTTTTTGCGGGTGTATCTTGACTGCGACGATATCACGAT | 785 |
| Db | 625 | CACAACTCTCCGCGCAACTTTTTGCGGGTGTATCTTGACTGCGACGATATCACGAT | 684 |
| Oy | 786 | CTCTTTTTCCGTCATCTGTTTCCGTGCTCCAAAACAAACAACGCGCGGGGAATTTCAAC | 845 |
| Db | 685 | CTCTTTTTCCGTCATCTGTTTCCGTGCTCCAAAACAAACAACGCGCGGGGAATTTCAAC | 744 |
| Oy | 846 | GAGCGTATCTGTCGGGAAGACCTGCGACACCTGCGAGAGATGTGTGGGTGTGAGACAA | 905 |
| Db | 745 | GAGCGTATCTGTCGGGAAGACCTGCGACACCTGCGAGAGATGTGTGGGTGTGAGACAA | 804 |
| Oy | 906 | GATGATTTCAATTACGGGGAGCCACCTGATAGCCTTTGTACTTAATCAGAGACTTCAG | 965 |
| Db | 805 | GATGATTTCAATTACGGGGAGCCACTGATAGCCTTTGTACTTAATCAGAGACTTCAG | 864 |
| Oy | 966 | GCGGTCAACGATGAAGAGGTGTGCTTTCGTTCCCAATGATATGTCTCCAGAAATGTAG | 1025 |
| Db | 865 | GCGGTCAACGATGAAGAGGTGTGCTTTCGTTCCCAATGATATGTCTCCAGAAATGTAG | 924 |
| Oy | 1026 | CCATCCATCTGTGTCATCAACAGCGTTGGTGCCTCCGGAATGTTTACATTAACGAGCAT | 1085 |
| Db | 925 | CCATCCATCTGTGTCATCAACAGCGTTGGTGCCTCCGGAATGTTTACATTAACGAGCAT | 984 |
| Oy | 1086 | AATCATAGACCTCTCACACAAGTTGCGCTCTTGTGATTAACGCGCAAGCTTTTCCGGT | 1145 |

| | | | |
|----|------|---|------|
| Db | 985 | AATCATATAGACCTCTCACACACAGTTGGCTCTTTGATTAACGCCACAGCTTTCCGGGT | 1044 |
| Qy | 1146 | ATCCAGATTCACAA - CCTTGCCTTCAAAAAATGAAACAATTTCACGACCGGCCGGTT | 1204 |
| Db | 1045 | ATCCAGATTCACAAACCTTGCTTCAAAAAATGAAACAATTTCACGACCGGCCGGTT | 1104 |
| Qy | 1205 | TATCATCCCCCTGGGGTGTAAATCAAAATAGCTGATGTACTCATGTAGGCCATATCTT | 1264 |
| Db | 1105 | TATCATCCCCCTGGGGTGTATCAAAATAGCTGATGTACTCATGTAGGCCATATCTT | 1164 |
| Qy | 1265 | GCCGTATCCCTGGAGATGGAACCTCTTGGCAACCGCTCCCGACCTTCCCTAGAGAGG | 1324 |
| Db | 1165 | GCCGTATCCCTGGAGATGGAACCTCTTGGCAACCGCTTCCCGACCTTCCCTAGAGAGG | 1224 |
| Qy | 1325 | GAGGCGCACAGAAAGCAATTCGTGTAAATTAGATTAATCGTATTTGTCAATCAGAGTGC | 1384 |
| Db | 1225 | GAGGCGCACAGAAAGCAATTCGTGTAAATTAGATTAATCGTATTTGTCAATCAGAGTGC | 1284 |
| Qy | 1385 | TTTTGGCAGAGAGAGATATGGGTTGGCACACAGCGCACCTTGAATCTTGTATCTT | 1444 |
| Db | 1285 | TTTTGGCAGAGAGAGATATGGGTTGGCACACAGCGCACCTTGAATCTTGTATCTT | 1344 |
| Qy | 1445 | GAAAGCTCCCTAGAAAACAGCTCTTCAATCTATATCAATTAACAGACTGGAATCCAC | 1504 |
| Db | 1345 | GAAAGCTCTCTAGAAAACAGCTCTTCAATCTATATCAATTAACAGACTGGAATCCAC | 1404 |
| Qy | 1505 | ATTATCAATATCCAGAGTATAGTAAACATTCGAAACCGTGAATGGAATGSAACAACCTTA | 1564 |
| Db | 1405 | ATTATCAATATCCAGAGTATAGTAAACATTCGAAACCGTGAATGGAATGSAACAACCTTA | 1464 |
| Qy | 1565 | AAATCGAGATATCCGGAATGATTTGATTTGCCAAAAATAGATCTCTGGCATGCGAATTC | 1624 |
| Db | 1465 | AAATCGAGATATCCGGAATGATTTGATTTGCCAAAAATAGATCTCTGGCATGCGAATTC | 1524 |
| Qy | 1625 | TCACGCGAGCGATTCATATGAGCGAGAGGACACCTTTTAGGAGACAGATAGATCCAGAG | 1684 |
| Db | 1525 | TCACGCGAGCGATTCATATGAGCGAGAGGACACCTTTTAGGAGACAGATAGATCCAGAG | 1584 |
| Qy | 1685 | AGTTCATGATAGTGCATATTCCTTGTCCCTATCGAAGAGACTCTGGACCAAAATCGTATTT | 1744 |
| Db | 1585 | AGTTCATGATAGTGCATATTCCTTGTCCCTATCGAAGAGACTCTGGACCAAAATCGTATTT | 1644 |
| Qy | 1745 | CATTAAAAACGGGAGGTAGATGAGATGACGAACGTGTACATGACTGAATCCCTGGT | 1804 |
| Db | 1645 | CATTAAAAACGGGAGGTAGATGAGATGACGAACGTGTACATGACTGAATCCCTGGT | 1704 |
| Qy | 1805 | AATCCGTTTGAATTCATCATATTAATTTTGGATGATTTGGAGACTTTTGTGCACTG | 1864 |
| Db | 1705 | AATCCGTTTGAATTCATCATATTAATTTTGGATGATTTGGAGACTTTTGTGCACTG | 1764 |
| Qy | 1865 | TCAAAATTTTGGAAACCCCTTTTGGAAACGAACACACGGTAGGGCTGGCAAAATGCCCA | 1924 |
| Db | 1765 | TCAAAATTTTGGAAACCCCTTTTGGAAACGAACACACGGTAGGGCTGGCAAAATGCCCA | 1824 |
| Qy | 1925 | TACTGTTGAGCAATTCAGTTCAATTAATATGTCTGCGGGCGCAACTGCACTCCGA | 1984 |
| Db | 1825 | TACTGTTGAGCAATTCAGTTCAATTAATATGTCTGCGGGCGCAACTGCACTCCGA | 1884 |
| Qy | 1985 | TAAATTAACGGCCCAACACCGGCATTAAGAAATGGAAGAGTTTTCACCTGCATACGACGA | 2044 |
| Db | 1885 | TAAATTAACGGCCCAACACCGGCATTAAGAAATGGAAGAGTTTTCACCTGCATACGACGA | 1944 |
| Qy | 2045 | TTCTGTGATTTGTATTCAGGCCCATATGCTTATAGCTTCGCAACCGAACCGACATTT | 2104 |
| Db | 1945 | TTCTGTGATTTGTATTCAGGCCCATATGCTTATAGCTTCGCAACCGAACCGACATTT | 2004 |
| Qy | 2105 | CGAAGTACTACGCGTAAGTATGTCAACTCGATATGTGCAATCTGTAAAAAGCAATTTTC | 2164 |
| Db | 2005 | CGAAGTACTACGCGTAAGTATGTCAACTCGATATGTGCAATCTGTAAAAAGCAATTTTC | 2064 |
| Qy | 2165 | CAGAACACAGGGGCTATCTCTTCAATAGCTTATGCAAGTTGCTCTCACCGGTTTCATCTT | 2224 |
| Db | 2065 | CAGAACACAGGGGCTATCTCTTCAATAGCTTATGCAAGTTGCTCTCACCGGTTTCATCTT | 2124 |

QY 2225 CCAGCGATAGATGGCGCGGCTTTCTTATGTTTGGGCTCCATGG 2278
 DB 2125 CCAGCGATAGATGGCGCGGCTTTCTTATGTTTGGGCTCCATGG 2178

RESULT 11
 ID ADJ25519/c
 ADJ25519 standard; DNA; 11004 BP.

ADJ25519;
 20-MAY-2004 (first entry)

ARE-LUC/CMV-rAR transgenic construct DNA sequence SEQ ID NO:1.

XX transgenic non-human mammal; androgen response element ; ARE;
 KW androgen receptor; transgenic mouse;
 KW selective androgen receptor modulator; SAR; cancer;
 KW defective androgen receptor function disorder; transgenic construct;
 KW ARE-LUC/CMV-rAR; gene; ds.

XX Synthetic.
 OS
 XX
 PN W02004007753-A2.
 XX
 PD 22-JAN-2004.
 XX
 PF 16-JUL-2003; 2003MO-US022142.
 XX
 PR 17-JUL-2002; 2002US-0396501P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Altar RM, Bol DK, Gottardis M, Mookhtiar K, Ostrowski J;
 PI Rowley RB;
 XX
 DR WPI; 2004-122974/12.

PT New transgenic non-human mammal expressing a reporter nucleic acid under
 PT the regulation of androgen response elements, useful as models for
 PT identifying and developing selective androgen receptor modulators for
 PT treating cancer.

XX
 PS Example; SEQ ID NO 1; 49pp; English.

XX The present invention describes a transgenic non-human mammal whose
 CC genome comprises a nucleic acid construct comprising a reporter nucleic
 CC acid encoding a reporter operably linked to a promoter comprising an
 CC androgen response element (ARE), and where the construct further
 CC comprises an androgen receptor nucleic acid encoding an androgen
 CC receptor, where expression of the reporter nucleic acid is regulated by
 CC expression of the androgen receptor nucleic acid. The mammal expresses
 CC the receptor nucleic acid in organs when the androgen receptor nucleic
 CC acid is expressed. Also described: (1) a cell isolated from the
 CC transgenic mouse, where the genome of the cell comprises the nucleic acid
 CC construct; (2) a mouse cell line comprising the cell of (1); (3) an
 CC isolated nucleic acid construct that comprises a reporter nucleic acid
 CC encoding a reporter operably linked to a promoter comprising an ARE; (4)
 CC obtaining a target mouse whose genome comprises the nucleic acid
 CC construct, where the mouse can be bred to produce progeny mice whose
 CC genomes comprise the nucleic acid construct; (5) producing a transgenic
 CC mouse cell line that expresses a reporter nucleic acid; and (6) screening
 CC for a modulator of the androgen receptor. The transgenic non-human mammal
 CC can be used as an in vivo model for the identification and development of
 CC selective androgen receptor modulators for the treatment of cancer or
 CC other disorders associated with defective androgen receptor functions.
 CC Selective androgen receptor modulators (SARMs) can act as antagonists or
 CC agonists in different tissues containing the androgen receptor. The
 CC present sequence represents a transgenic construct designated ARE-LUC/CMV
 CC -rAR, which is used in the exemplification of the present invention.

XX Sequence 11004 BP; 2793 A; 2573 C; 2621 G; 3017 T; 0 U; 0 Other;

Query Match 60.0%; Score 1663.4; DB 12; Length 11004;
 Best Local Similarity 97.4%; Pred. No. 5.1e-214;
 Matches 1691; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 542 AAAGGAAATGCTTAAGAG 601
 DB 4385 ATATAACATGAATTTTATCAATAGCGAAAAAGAAACAATCAGAGGTCCCAAACTCAC 4326
 QY 602 GCCGAGTCTTAACCCCACTTTAAACGGCGATCTTCGCGCTTGGCTTATGA 661
 DB 4325 CCGAAGTCTCAGCTTAGAAATACCGCGCATCTTTCGCGCTTCTTATGA 4266
 QY 662 GGATCTCTGATTTTCTTGGGTCGAGTTTCCGGTAAAGACTTTCGGTACTCTGCA 721
 DB 4265 GGATCTCTGATTTTCTTGGGTCGAGTTTCCGGTAAAGACTTTCGGTACTCTGCA 4206
 QY 722 CAAACCAACTCTCTCGCGCAACTTTTTCGGGTTGTTACTGACTGCGAGTAATCA 781
 DB 4205 CAAACCAACTCTCTCGCGCAACTTTTTCGGGTTGTTACTGACTGCGAGTAATCA 4146
 QY 782 CGATCTCTTTTCCGTCATGCTCTTCCGTCCTCCAAACCAACGCGCGGGAAGTT 841
 DB 4145 CGATCTCTTTTCCGTCATGCTCTTCCGTCCTCCAAACCAACGCGCGGGAAGTT 4086
 QY 842 CACCGGCTCATGTCGGGAAAGCTGCGACACCTGCGTAAGATGTTGGGTTTGA 901
 DB 4085 CACCGGCTCATGTCGGGAAAGCTGCGACACCTGCGTAAGATGTTGGGTTTGA 4026
 QY 902 GCAGATGATTCCTCAATTCAGCGGAGCCACTGATAGCTTGTACTTAATCAGACT 961
 DB 4025 GCAGATGATTCCTCAATTCAGCGGAGCCACTGATAGCTTGTACTTAATCAGACT 3966
 QY 962 TCAGCGGTCACAGTAAGAGTGTGCTTCGTCGCAAGGATGTCCTCCGAAT 1021
 DB 3965 TCAGCGGTCACAGTAAGAGTGTGCTTCGTCGCAAGGATGTCCTCCGAAT 3906
 QY 1022 GTAGCCATCATCTTGTCAATCAAGCGCTGTGCTTCGGATTGTTTACATACCG 1081
 DB 3905 GTAGCCATCATCTTGTCAATCAAGCGCTGTGCTTCGGATTGTTTACATACCG 3846
 QY 1082 ACATTAATCATAGAGCTCTCAACACAGTTCCGCTTGTGATTAACGCCAGCTTTCC 1141
 DB 3845 ACATTAATCATAGAGCTCTCAACACAGTTCCGCTTGTGATTAACGCCAGCTTTCC 3786
 QY 1142 CGGTATCCAGATCCAAACCTTCGCTTCAAAAATGGAACAACCTTACCGACCGCGCCG 1201
 DB 3785 CGGTATCCAGATCCAAACCTTCGCTTCAAAAATGGAACAACCTTACCGACCGCGCCG 3726
 QY 1202 GTTATCATCCCTCGGCTGTATCAGATAGCTGATGTAGTCTCAGTAGCCATATC 1261
 DB 3725 GTTATCATCCCTCGGCTGTATCAGATAGCTGATGTAGTCTCAGTAGCCATATC 3666
 QY 1262 CTTCCTGATACCTGCGAGATGGAACCTTTGGCAACCGCTTCCGACTTCTTGAAG 1321
 DB 3665 CTTCCTGATACCTGCGAGATGGAACCTTTGGCAACCGCTTCCGACTTCTTGAAG 3606
 QY 1322 GGGGAGCGCCACAGAGGAATTCGTGTAATTAATGATTAATGTTGTCAATCAGAG 1381
 DB 3605 GGGGAGCGCCACAGAGGAATTCGTGTAATTAATGATTAATGTTGTCAATCAGAG 3546
 QY 1382 TGGTTTGGCGAAGAGAAATAGGGTTGGACACGACGCACTTTGAATCTTGAAT 1441
 DB 3545 TGGTTTGGCGAAGAGAAATAGGGTTGGACACGACGCACTTTGAATCTTGAAT 3486
 QY 1442 CCGAAGGCTCTCAGAAACAGCTCTTCTTCAATTTATTAAGACGACTCGAAATC 1501
 DB 3485 CCGAAGGCTCTCAGAAACAGCTCTTCTTCAATTTATTAAGACGACTCGAAATC 3426
 QY 1502 CACATATCAAAATTCGAGATGTAAGTAACATTCGAAACCGGATGGAATGGAACAAC 1561
 DB 3425 CACATATCAAAATTCGAGATGTAAGTAACATTCGAAACCGGATGGAATGGAACAAC 3366

Db 1773 TGCTCGAAGCGGCGCGCGCCGCACTCTAGAAATTACAGCGGATCTTTCCGCCCTTCTT 1714
 Qy 651 GGCCTTATGAGATCTCTGATTTTTCTGCGTCGAGTTTCCGGTAAGACCTTTCCG 710
 Db 1713 GGCCTTATGAGATCTCTGATTTTTCTGCGTCGAGTTTCCGGTAAGACCTTTCCG 1654
 Qy 711 TACTTGTCCCAACCAACTCTCCGCGCACTTTTGGCGGTTGTACTGACTGGC 770
 Db 1653 TACTTGTCCCAACCAACTCTCCGCGCACTTTTGGCGGTTGTACTGACTGGC 1594
 Qy 771 GACGTATCCAGATCTCTTTTCCGTCATGTCCTTTCCGTCGCAAAAACAACAGGC 830
 Db 1593 GACGTATCCAGATCTCTTTTCCGTCATGTCCTTTCCGTCGCAAAAACAACAGGC 1534
 Qy 831 GCGCGGAAGTTCAACCGCGTCATGTCGCGAAGACTCGCAACCTCGTCGAGATGT 890
 Db 1533 GCGCGGAAGTTCAACCGCGTCATGTCGCGAAGACTCGCAACCTCGTCGAGATGT 1474
 Qy 891 GGGGTGTTGAGCAAGATGATTCATTCAGCGGAGCCACTGATAGCTTTGTACTT 950
 Db 1473 GGGGTGTTGAGCAAGATGATTCATTCAGCGGAGCCACTGATAGCTTTGTACTT 1414
 Qy 951 AATCAGAGACTTCAGGCGGTCAACGATGAAGAAGTTCGTCCTCCGTCGAGTAAGCTAT 1010
 Db 1413 AATCAGAGACTTCAGGCGGTCAACGATGAAGAAGTTCGTCCTCCGTCGAGTAAGCTAT 1354
 Qy 1011 GTCTCCGAAGTGAAGCCATCATCTTGTCAATCAGCGGTCGCTTCGGATTTGT 1070
 Db 1353 GTCTCCGAAGTGAAGCCATCATCTTGTCAATCAGCGGTCGCTTCGGATTTGT 1294
 Qy 1071 TACTTAACCGGACATTAATCATAGAGCTCTCACAACAAGTTCCGCTCTTTGATTAACGCC 1130
 Db 1293 TACTTAACCGGACATTAATCATAGAGCTCTCACAACAAGTTCCGCTCTTTGATTAACGCC 1234
 Qy 1131 CAGCGTTTCCCGGTATCCAGATCCACAACCTTGCTTCAAAAAATGGAACAACTTACC 1190
 Db 1233 CAGCGTTTCCCGGTATCCAGATCCACAACCTTGCTTCAAAAAATGGAACAACTTACC 1174
 Qy 1191 GACCGCGCCCGGTTTATCATCCCTCGGTTGTAATCAGAAATAGCTGATGTCAGT 1250
 Db 1173 GACCGCGCCCGGTTTATCATCCCTCGGTTGTAATCAGAAATAGCTGATGTCAGT 1114
 Qy 1251 GACGCCATATCTCTTGCTGATCCTGGCAGATGGAACCTCTTGCAACCGCTTCCCGAC 1310
 Db 1113 GACGCCATATCTCTTGCTGATCCTGGCAGATGGAACCTCTTGCAACCGCTTCCCGAC 1054
 Qy 1311 TTCTTATGAGAGGAGCGCCACACAGAACTTCGTGTAATTAAGTAATCGTATTT 1370
 Db 1053 TTCTTATGAGAGGAGCGCCACACAGAACTTCGTGTAATTAAGTAATCGTATTT 994
 Qy 1371 GTCATCAGAGTCTTTTGGCGAAGAAAGAAATAGGTTGGACACGACGCGCATTTTG 1430
 Db 993 GTCATCAGAGTCTTTTGGCGAAGAAAGAAATAGGTTGGACACGACGCGCATTTTG 934
 Qy 1431 AATCTTGTATCTCTGAAGGCTCTCTCAGAAACAGCTCTTCTTCAATCTTAACCTTAAGAC 1490
 Db 933 AATCTTGTATCTCTGAAGGCTCTCTCAGAAACAGCTCTTCTTCAATCTTAACCTTAAGAC 874
 Qy 1491 GACTCGAAATCCATATCAATATCCGAGTATGAATTAACATTCAAAACCGGATGGAA 1550
 Db 873 GACTCGAAATCCATATCAATATCCGAGTATGAATTAACATTCAAAACCGGATGGAA 814
 Qy 1551 TGGAAACAACCTTAAATCGCAGTATCCGAAATGATTTGATTCGAAAAATAGATCTCT 1610
 Db 813 TGGAAACAACCTTAAATCGCAGTATCCGAAATGATTTGATTCGAAAAATAGATCTCT 754
 Qy 1611 GGCATGGAATAATCTCAGCAGGAGTTCTATGAGGACAGCGACACTTTAGCAGACC 1670
 Db 753 GGCATGGAATAATCTCAGCAGGAGTTCTATGAGGACAGCGACACTTTAGCAGACC 694
 Qy 1671 AGTAGATCCAGAGAGTTTCAATGATGAGTATGCTTGTCCCTATCGAAGGACTCTGG 1730
 Db 693 AGTAGATCCAGAGAGTTTCAATGATGAGTATGCTTGTCCCTATCGAAGGACTCTGG 634

Qy 1731 CACAAATCGTATTCATTAATAACGGGAGTAGATGAGTACGAACTGTACATCGA 1790
 Db 633 CACAAATCGTATTCATTAATAACGGGAGTAGATGAGTACGAACTGTACATCGA 574
 Qy 1791 CTGAAATCCCTGGTATCCGTTTATGATTCATGATTAATATTTTGGATGGAG 1850
 Db 573 CTGAAATCCCTGGTATCCGTTTATGATTCATGATTAATATTTTGGATGGAG 514
 Qy 1851 CTTTATTTGACGTTCAAAATTTTGGAAACCCCTTTTGGAAACGACCGGATGG 1910
 Db 513 CTTTATTTGACGTTCAAAATTTTGGAAACCCCTTTTGGAAACGACCGGATGG 454
 Qy 1911 CTGGAATGCCCATCTGTTGAGCAATTCACGTTCAATTAATATGTCGTCGGGCGC 1970
 Db 453 CTGGAATGCCCATCTGTTGAGCAATTCACGTTCAATTAATATGTCGTCGGGCGC 394
 Qy 1971 AACTGCAACTCCGATTAATTAACCGGCCCAACCGGATTAAGAAATGAAGATTTTC 2030
 Db 393 AACTGCAACTCCGATTAATTAACCGGCCCAACCGGATTAAGAAATGAAGATTTTC 334
 Qy 2031 ACTGCATAGAGATTCGTGATTTGATTAATCAGCCATATCGTTGATAGCTTCTGCAA 2090
 Db 333 ACTGCATAGAGATTCGTGATTTGATTAATCAGCCATATCGTTGATAGCTTCTGCAA 274
 Qy 2091 CCGAAGGACATTTGGAAGTACTCAGCGTAAGTATGTCACCTCGATATGTCATCTGT 2150
 Db 273 CCGAAGGACATTTGGAAGTACTCAGCGTAAGTATGTCACCTCGATATGTCATCTGT 214
 Qy 2151 AAAAGCAATTTGTTCCAGAAACGAGGCGTATCTCTTCAATAGCTTATGCACTTCTCC 2210
 Db 213 AAAAGCAATTTGTTCCAGAAACGAGGCGTATCTCTTCAATAGCTTATGCACTTCTCC 154
 Qy 2211 AGCGGTTCCATCTTCCAGGAGATGAATGGCGCGGCGCTTCTTATATGTTTGGCGTC 2270
 Db 153 AGCGGTTCCATCTTCCAGGAGATGAATGGCGCGGCGCTTCTTATATGTTTGGCGTC 94
 Qy 2271 TTCCATGG 2278
 Db 93 TTCCATGG 86

RESULT 13
 AAA29136/c
 ID AAA29136 standard; DNA; 4987 BP.
 XX
 AC AAA29136;
 XX
 DF 12-SEP-2000 (first entry)
 XX
 DE pNF-kappaB-luc construct.
 XX
 KW Vector; transcription; cis-element; nuclear factor-kappaB; NF-kappaB;
 KW luc; luciferase; reporter; promoter; monitor; signal transduction; ss.
 XX
 OS Synthetic.
 XX
 PN W0200034435-A2.
 XX
 PD 15-JUN-2000.
 XX
 PF 01-DEC-1999; 99WO-US028451.
 XX
 PR 08-DEC-1998; 98US-00206887.
 XX
 PA (CLON-) CLONTECH LAB INC.
 XX
 PI Li X, Zhao X, Jiang X, Fang Y, Duong T, Kain S;
 XX
 DR MPI; 2000-423400/36.
 XX
 PT cis element-reporter construct for measuring transcription, comprises a
 reporter gene, promoter and a cis element such as nuclear factor-kappaB.

AC ABV73856;
 XX
 DT 29-AUG-2003 (revised)
 DT 08-JAN-2003 (first entry)
 XX
 DE Plasmid pNFkB-Luc.
 XX
 KW Screening; cell-based assay; cellular target; firefly; luciferase;
 KW reporter; pNFkB-Luc; gene; ds.
 XX
 OS Photinus pyralis.
 OS Herpes simplex virus.
 OS Chimeric.
 XX
 PN W0200272783-A2.
 XX
 PD 19-SEP-2002.
 XX
 PF 12-MAR-2002; 2002WO-US007713.
 XX
 PR 12-MAR-2001; 2001US-0275266P.
 XX
 PA (IRMT-) IRM LLC.
 PI Caldwell JS, Chanda SK, Somia NV, Hogenesch JB, Cooke MP;
 PI Aza-Blanc P;
 XX
 DR WPI; 2002-750492/81.
 XX
 PT Identifying targets of effectors of gene expression or cellular activity,
 PT by contacting reporter cells with an effector, adding nucleic acid
 PT encoding a target and identifying cells with altered expression or
 PT activity.
 XX
 XX Example 1; Page 130-132; 140pp; English.
 XX
 CC The present sequence is that of pNFkB-Luc, a plasmid designed for
 CC monitoring the activation of the NFkB signal transduction pathway. The
 CC plasmid contains the firefly luciferase (luc) gene (E354K mutant), and 4
 CC tandem copies of the NFkB consensus sequence fused to a TAT-like promoter
 CC from the herpes simplex virus thymidine kinase gene. A 1912 bp segment of
 CC the plasmid containing the NFkB consensus sequences, the promoter and the
 CC luciferase coding sequence was amplified by PCR (see ABV73854-55) and
 CC cloned into the XhoI and BamHI sites of the SIN retroviral reporter
 CC vector, producing SKB-N. The vector was used for stable reporter cell
 CC generation in an example of the invention. The invention provides cell-
 CC based screening methods for identifying the targets of effectors or
 CC modulators of gene expression or cellular activity. The effect of a small
 CC molecule or other signal on a reporter cell is titrated by expressing
 CC within the cell cDNA that encodes a polypeptide that is the molecular
 CC target or that is responsible for directly or indirectly producing the
 CC molecular target. The method permits identification of gene function by
 CC modulating the level of message. NFkB reporter cells in a multiwell plate
 CC can be used. The method is fully automated and provides an increased
 CC throughput over conventional methods. Miniaturization and automation of
 CC transfection/transduction procedures permit comprehensive studies of
 CC phenotypes or pathways at the level of genome. (updated on 29-AUG-2003 to
 CC standardise OS field)
 CC
 XX
 SQ Sequence 4987 BP; 1295 A; 1188 C; 1207 G; 1297 T; 0 U; 0 Other;
 Query Match 59.8%; Score 1657.6; DB 6; Length 4987;
 Best Local Similarity 98.9%; Pred. No. 3.3e-213;
 Matches 1663; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 591 TGGCCTTAAGAGCGGAGTGTTCACCACTTTAAACGGCGATCTTTCCGCCCTTCTT 650
 Db 1942 TGTCTCGAAGCGGCGCGCCGCCGACCTGATTAACAGCGGATCTTTCCGCCCTTCTT 1883
 QY 651 GGGCTTTATAGAGATCTCTGATTTTCTTGCGTGAAGTTTCCGTAAGACCTTTCCG 710
 Db 1882 GGGCTTTATAGAGATCTCTGATTTTCTTGCGTGAAGTTTCCGTAAGACCTTTCCG 1823

QY 711 TACTGTCCAGAAACAATCTCCGCGCACTTTTCCGGTTGTTACTTGAAGTGGC 770
 Db 1822 TACTGTCCAGAAACAATCTCTCCGCACTTTTCCGGTTGTTACTTGAAGTGGC 1763
 QY 771 GAGTAATCCAGATCTCTTTTCCGTCATCGTCTTCCGTCGCAAAAACAACGAGC 830
 Db 1762 GAGTAATCCAGATCTCTTTTCCGTCATCGTCTTCCGTCGCAAAAACAACGAGC 1703
 QY 831 GCGGGGAAGTTCAACCGGCGTCATGTCGGGAGAACCTGCGACCTGCGTGAAGTGT 890
 Db 1702 GCGGGGAAGTTCAACCGGCGTCATGTCGGGAGAACCTGCGACCTGCGTGAAGTGT 1643
 QY 891 GGGGTGTGAGGAAGATGGAATTCATTGAGGGAGCCACCTGATAGCTTGTACTT 950
 Db 1642 GGGGTGTGAGGAAGATGGAATTCATTGAGGGAGCCACCTGATAGCTTGTACTT 1583
 QY 951 AATCAGAGATTCAGGCGGTCAACGATGAAGATGTCCTTCTGTCAGTAAGCTAT 1010
 Db 1582 AATCAGAGATTCAGGCGGTCAACGATGAAGATGTCCTTCTGTCAGTAAGCTAT 1523
 QY 1011 GTCTCCAGATGTAAGCATTCATCTTGTCAATCAAGGCTTGTGCGATTGTT 1070
 Db 1522 GTCTCCAGATGTAAGCATTCATCTTGTCAATCAAGGCTTGTGCGATTGTT 1463
 QY 1071 TACATAACGGAGATATATATATAGACCTTCACACAGTGGCTTTGATTAAAGCC 1130
 Db 1462 TACATAACGGAGATATATATATAGACCTTCACACAGTGGCTTTGATTAAAGCC 1403
 QY 1131 CAGCGTTTCCCGATTCAGATCAACAACCTTCCGTTCAAAAATGGAACAACCTTACC 1190
 Db 1402 CAGCGTTTCCCGATTCAGATTCAGATCAACAACCTTCCGTTCAAAAATGGAACAACCTTACC 1343
 QY 1191 GACCGCGCGGTTTATCATCCCTCGGGTGAATGAGATGCTGATGTCAGT 1250
 Db 1342 GACCGCGCGGTTTATCATCCCTCGGGTGAATGAGATGCTGATGTCAGT 1283
 QY 1251 GAGCCCATATCTCTGCTGATACCTGAGATGGAACCTTGGCAACCGCTTCCCGAGC 1310
 Db 1282 GAGCCCATATCTCTGCTGATACCTGAGATGGAACCTTGGCAACCGCTTCCCGAGC 1223
 QY 1311 TTCCTTAGAGAGGAGCGCCACACAGAACCAATTCGTGAATTTGATTAATCGTATTT 1370
 Db 1222 TTCCTTAGAGAGGAGCGCCACACAGAACCAATTCGTGAATTTGATTAATCGTATTT 1163
 QY 1371 GTCAATCAAGTCTTTTGGCGAAGAGATGAGTTGGACCAAGCGCATTTTG 1430
 Db 1162 GTCAATCAAGTCTTTTGGCGAAGAGATGAGTTGGACCAAGCGCATTTTG 1103
 QY 1431 AATCTGTATCTGTAAGGCTCTCAGAAACAGCTTCTTCAAACTATATATTAAGAC 1490
 Db 1102 AATCTGTATCTGTAAGGCTCTCAGAAACAGCTTCTTCAAACTATATATTAAGAC 1043
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 Qy 2151 AAAAGCAATTTTCCAGAACACGAGGCTATCTTTCATAGCCTTATGAGTTGCTTCC 2210
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 DT 11-DEC-2002 (first entry)
 DE Human inducibly regulated gene promoter associated vector #1.
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 XX biosensor; reporter gene construct; vector; ds; circular; cyclic.
 OS Synthetic.
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 PN WO200272789-A2.
 PD 19-SEP-2002.
 XX
 PF 12-MAR-2002; 2002WO-US008008.
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 PR 12-MAR-2001; 2001US-0274979P.
 PR 12-MAR-2001; 2001US-0275070P.
 PR 12-MAR-2001; 2001US-0275148P.
 PA (IRMI-) IRM LLC.
 PI Caldwell JS, Su AI, Hogenesch JB;
 XX
 DR MPI; 2002-723339/78.
 XX
 PT Producing a collection of responder cells for high throughput screening
 PT assays, comprises identifying and cloning regulatory regions into
 PT expression constructs to control nucleic acids, and introducing into
 PT addressable cells.
 PS Disclosure; Page 177-178; 187pp; English.

XX The invention describes producing a collection of responder cells for
 CC high throughput screening assays, by identifying and cloning regulatory
 CC regions into expression constructs to control nucleic acids, and
 CC introducing the constructs into addressable cells. The method is useful
 CC in producing cells used in high throughput screening assays for profiling
 CC substances and conditions and for studying the function of the regulatory
 CC region mediating the response. The cells serve as biosensors to assess
 CC the effects of any perturbation, such as external or internal condition,
 CC on the cells from which the regulatory regions in the reporter gene
 CC constructs are derived can be inferred. This sequence represents a vector
 CC useful for the delivery of reporter gene constructs into cells
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 Qy 1371 GTCAATCAGAGTCTTTTGGCGAAGAGAGATAGGTTGGCACACAGCGCACTTGG 1430

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QY 1431 AATTTTGTATCTGGAAGGCTCTCAGAAAACAGCTCTTCTCAATCTATACATTAAAGAC 1490
Db 1102 AATCTGTAACTCGAAGGCTCCTCAGAAAACAGCTCTTCTCAATCTATACATTAAAGAC 1043
QY 1491 GACTCGAAATCCACATATCAAAATATCCGAGTGTAGTAAACATTCAAAACCGTGAATGAA 1550
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Search completed: September 29, 2005, 15:00:48
Job time : 1455 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2005, 11:18:47; Search time 8765 Seconds
(without alignments)
12033.781 Million cell updates/sec

Title: US-10-734-801-18

Perfect score: 2771

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gsa1: *
9: gb_gsa2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 2 | 914.6 | 33.0 | 1032 | 8 | BZ675132 PUBR187TD |
| C 3 | 871.8 | 31.5 | 973 | 8 | BZ701200 PUBMP50TD |
| C 4 | 861.2 | 31.1 | 949 | 8 | BZ681727 PUBH142TD |
| C 5 | 852.8 | 30.8 | 944 | 8 | BZ672965 PUBGP25TD |
| C 6 | 831.6 | 30.0 | 902 | 8 | BZ670418 PUBH17TD |
| C 7 | 827.4 | 29.9 | 929 | 8 | BZ678861 PUBR69TD |
| C 8 | 811.8 | 29.3 | 911 | 8 | BZ671975 PUBR85TD |
| C 9 | 809.8 | 29.2 | 885 | 8 | BZ686758 PUBR30TD |
| C 10 | 804.8 | 29.0 | 884 | 8 | BZ703458 PUBR00TD |
| C 11 | 795.4 | 28.7 | 866 | 8 | BZ679896 PUBR13TD |
| C 12 | 793.2 | 28.7 | 866 | 8 | BZ682015 PUBR02TD |
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| C 14 | 793.4 | 28.6 | 882 | 8 | BZ682835 PUBR67TD |
| C 15 | 787.6 | 28.4 | 867 | 8 | BZ683904 PUBH05TD |
| C 16 | 760.8 | 27.5 | 863 | 8 | BZ676173 PUBR16TD |
| C 17 | 748.4 | 27.0 | 814 | 8 | BZ685628 PUBR19TD |
| C 18 | 738.8 | 26.7 | 822 | 8 | BZ682928 PUBR00TD |
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ALIGNMENTS

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VERSION BZ676934.1
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SOURCE Zea mays
ORGANISM Zea mays
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Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1034)
Whiteley,C.A., Quackenbush,J., Van Aken,S., Uteerback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennerzen,J.
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
JOURNAL Contact: Cathy Whiteley
COMMENT TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteley@tigr.org
Seq primer: TIF
Classes: sheared ends.

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Matches 973; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

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LOCUS PUBIG87TD ZM_0_6_1_0_KB Zea mays genomic clone ZMBRta061P05,
DEFINITION

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VERSION        B2675132.1  GI:28225738
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AUTHORS        Whiteley,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
                Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                Bennetzen,J.
TITLE          Maize Genomics Consortium
JOURNAL        Unpublished (2003)
COMMENT        Contact: Cathy Whiteley
                TIGR
                9712 Medical Center Drive, Rockville, MD 20850, USA
                Tel: 301-838-5843
                Fax: 301-838-0208
                Email: whiteley@tigr.org
                Seq primer: TF
                Class: sheared ends.
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 Db 605 GCTTCCCGACTCTCTTAGAGAGAGCGCCCGCCAGAGCAATTCGTGTAATTAAT 664
 QY 1360 AAATCGTATTTGTCAATCAGAGTGTCTTTGGCGAAGAGAGATAGGTTTGGCA 1419
 Db 665 AAATCGTATTTGTCAATCAGAGTGTCTTTGGCGAAGAGATAGGTTTGTACTAG 724
 QY 1420 AGCGCACTTGAATCTTGTAACTCTGAAAGCTCTCAAGAAAGCTCTTCTCAATCT 1479
 Db 725 AAGCGACTTTGAAATTTGTAACTCTGAAAGAGTCTTAAACAGCTCTTCTCAATCT 784
 QY 1480 TACATTTAAGACGACTCGAAATCCATATCAATATCCAGTGTAGTAAACATTC 1539
 Db 785 TACATTTAAGACGACTCGAAATCCATATCAATATCCAGTGTAGTAAACATTC 844
 QY 1540 CCGTATGGAATGGAACAACACTTAAATCCGAGATCCGGAATGATTGATTCGCA 1599
 Db 845 CCGTATGGAATGGAACAACACTTAAATCCGAGATCCGGAATGATTGATTCGCA 904
 QY 1600 ATAGATCTCTGCGCATGCGAATCTCAGCGAGCGATTTCTATGAGCGAGACGAC 1659
 Db 905 ATAGATCTCTGCGCATGCGAATCTCAGCGAGCGATTTCTATGAGCGAGACGAC 963
 QY 1660 TTAGGACAGCCAGTATGATCCAGAGAGTTCATGATCAGTCAATGTCTGTCCCTAT 1719
 Db 964 CTAGGTAACCCAGTATGATCCAGAGAGTTCATGATCAGTCAATGTCTGTCCCTAT 1023
 QY 1720 AAGGACTCT 1728
 Db 1024 AAGGACTCT 1032

RESULT 3
 LOCUS BZ701200/c 973 bp DNA linear GSS 19-FEB-2003
 DEFINITION PUBM587D_ZM_0.6.1.0_XB_Zea_mays genomic clone ZM587A089304,
 genomic survey sequence.
 ACCESSION BZ701200
 VERSION BZ701200.1 GI:28421047
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE
 AUTHORS White, J., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Benneken, J.
 TITLE Maize Genomics Consortium
 JOURNAL Unpublished (2003)
 COMMENT Contact: Cathy White, Tel: 301-838-5843 Fax: 301-838-0208 Email: whitec@maizegenomics.org
 Seq primer: TP
 Class: sheared ends.

FEATURES
 source location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="B73"
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 /clone="ZM587A089304"

/clone.lib="ZM_0.6.1.0_KB"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
 Cor selected genomic DNA library"

ORIGIN
 Query Match 31.5%; Score 871.8; DB 8; Length 973;
 Best Local Similarity 95.0%; Pred. No. 9.4e-168;
 Matches 900; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

1330 CCACCAAGACAAATTCGTGTAATTAATGATTAATGTTGTCAATCAGAGTCTTTG 1389
 Db 961 CCCCCAGAGCAATTCGTGTAATTAATGATTAATGTTGTCAATCAGAGTCTTTG 902
 QY 1390 GCGAAGAGGAAATAGGTTTGGACCGCGAGCGCACTTGAATGTTAAATCCGAAG 1449
 Db 901 GCGAAGAGGAAATAGGTTTGGACCGCGAGCGCACTTGAATGTTAAATCCGAAG 842
 QY 1450 CTCCTCAGAAACAGCTCTTCTTCAATCTATACATTAAGACGACTCGAAATCCATATC 1509
 Db 841 GATGTAATAACAGCTCTTCTTCAATCTATACATTAAGACGACTCGAAATCCATATC 782
 QY 1510 AAATATCCGAGTGTAAACATTCGAAACCGGATGGAATGGAACAACCTTAAATC 1569
 Db 781 AAATATCCGAGTGTAAACATTCGAAACCGGATGGAATGGAACAACCTTAAATC 722
 QY 1570 GCAGATCCGGAATGATTTGATTCGCAAAATAGGATCTCGGACATGGAGATCTACG 1629
 Db 721 GCAGATCCGGAATGATTTGATTCGCAAAATAGGATCTCGGACATGGAGATCTACG 662
 QY 1630 CAGGAGTTCTATGAGCGAGACGACCTTTAGCGAGACGATGATCCAGAGAGTTTC 1689
 Db 661 CAGGAGTTCTATGAGCGAGACGACCTTTAGCGAGACGATGATCCAGAGAGTTTC 602
 QY 1690 ATGATCAGTGAATGTCTTGTCTCTATCGAAGACTCTGCACAAAATCGATTCAAT 1749
 Db 601 ATGATCAGTGAATGTCTTGTCTCTATCGAAGACTCTGCACAAAATCGATTCAAT 542
 QY 1750 AAACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1809
 Db 541 AAACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482
 QY 1810 GTTTAGATCATGATATATATTTTGTGATGATGATGATGATGATGATGATGATGAT 1869
 Db 481 GTTTAGATCATGATATATATTTTGTGATGATGATGATGATGATGATGATGATGAT 422
 QY 1870 ATTTTGTGCAACCCCTTTTGGAAACGAACCAACGATAGCTGCGAATGCCATCTG 1929
 Db 421 ATTTTGTGCAACCCCTTTTGGAAACGAACCAACGATAGCTGCGAATGCCATCTG 362
 QY 1930 TTGACCAATTCAGTTCATTAATATGCTGCTGCGGCGGCACTGCAATCCGATTAAT 1989
 Db 361 TTGACCAATTCAGTTCATTAATATGCTGCTGCGGCGGCACTGCAATCCGATTAAT 302
 QY 1990 AACGCGCCCAACCGGAGATTAAGATTAAGAGATTTTCACTGATACGACGATCTG 2049
 Db 301 AACGCGCCCAACCGGAGATTAAGATTAAGAGATTTTCACTGATACGACGATCTG 242
 QY 2050 TGATTTGATTCAGCCATATCGTTTCATATGCTTTCGCAACGAAACGACATTTGAA 2109
 Db 241 TGATTTGATTCAGCCATATCGTTTCATATGCTTTCGCAACGAAACGACATTTGAA 182
 QY 2110 TACTCAGCGTAAGATGATTCACCTCGCATATGATGATCTGTAAAGCAATGTTCCAGA 2169
 Db 181 TACTCAGCGTAAGATGATTCACCTCGCATATGATGATCTGTAAAGCAATGTTCCAGA 122
 QY 2170 ACCAGGCGTATCTCTCATAGCTTATGAGAGTTGCTCCAGCGGTTCCATCTCCAGC 2229
 Db 121 ACCAGGCGTATCTCTCATAGCTTATGAGAGTTGCTCCAGCGGTTCCATCTCCAGC 62
 QY 2230 GGATGAGATGCGCGCGGCTTTCTTAAATGTTTGGGCTTCCAT 2276
 Db 61 GGATGAGATGCGCGCGGCTTTCTTAAATGTTTGGGCTTCCAT 15

RESULT 4
 BZ681727/c 949 bp DNA linear GSS 05-FEB-2003
 LOCUS PUBH142T.ZM_0.6_1.0_KB Zea mays genomic clone ZMBRta05SH1,
 DEFINITION genomic survey sequence.
 BZ681727
 ACCESSION BZ681727.1 GI:28237508
 VERSION GSS.
 KEYWORDS Zea mays
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 949)
 WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Bennettzen,J.
 TITLE Maize Genomics Consortium
 JOURNAL Unpublished (2003)
 COMMENT Contact: Cathy WhiteLaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteLaw@tigr.org
 Seq primer: TP
 Class: sheared ends.

FEATURES
 Source
 Location/Qualifiers
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 /organism="Zea mays"
 /mol_type="genomic DNA"
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 /db_xref="taxon:4577"
 /clone="ZMBRta05SH1"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
 Cot selected genomic DNA library"

ORIGIN
 Query Match 31.1%; Score 861.2; DB 8; Length 949;
 Best Local Similarity 94.9%; Pred. No. 1,4e-165;
 Matches 890; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

1344 TTGCGTAAATTGATGATTAATCGTATTTGCAATCAGAGTCTTTGGCCGAAGAGGAA 1403
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 1404 TAGGGTTGGCAGCAGCAGCGCACTTGAATCTTGTAATCCTGAAGGCTCCTCAGAAACAG 1463
 889 TAGGGTTGGTACTAGCAAGCAGCACTTTGAATCTTGTAATCCTGAAGGATGTAATAACAG 830
 1464 CTTTCTTCAAACTATACATTAAAGAGATCGAATCCGATATCAAAATATCCGAGTGT 1523
 829 CTTCTTCTTCAAACTATACATTAAAGAGATCGAATCCGATATCAAAATATCCGAGTGT 770
 1524 AGTAACATTCCAAAACCGGATGAGATGGAACAACCTTAATATGCGAGTATCCGGAAT 1583
 769 AGTAACATTCCAAAACCGGATGAGATGGAACAACCTTAATATGCGAGTATCCGGAAT 710
 1584 GATTGATTTGCCAAAATAGAGATCTCTGGCATCGAGAAATCTGACGAGCACTTTATAG 1643
 709 GATTGATTTGCCAAAATAGAGATCTCTGGCATCGAGAAATCTGACGAGCACTTTATAG 650
 1644 AGCGAAGGCGACACCTTTAGGACAGACAGTAGATCCAGAGAGTTGATGATCAGTCCAA 1703
 649 CGGAAGGCGACACCTTTAGTAAACCAAGTAGATCCAGAGAGTTGATGATCAGTCCAA 590
 1704 TGCTCTTGCCATTCAGAGAGCTCTGGCAGCAAAATGATATCATTTAAACCGGAGAGTAG 1763
 589 TGCTCTTGCCATTCAGAGAGCTCTGGTAAACAAATGATATCATTTAAACCGGAGAGTAG 530
 1764 ATGAGATGTGACGAAGGTGATACGATGAATCCCTGGTATTCGTTTAAATCCAT 1823

Db 529 ATGAGATGTGACGAAGGTGATACGATGAATCCCTGGTATCCGTTTAAATCCAT 470
 Qy 1824 GATTAATATTTTGGATGAGAGCTTTTGGACAGTTCAAAATTTTGGCAACC 1883
 Db 469 GATTAATATTTTGGATGAGAGCTTTTGGACAGTTCAAAATTTTGGCAACC 410
 Qy 1884 CTTTGGAAACGAACACACCGGTAGCTGCGAAATGCCCATCTTTGAGCAATTACG 1943
 Db 409 CTTTGGAAACGAACACACCGGTAGCTGCGAAATGCCCATCTTTGAGCAATTACG 350
 Qy 1944 TTCAATTAATAGTCTGTTGCGCGGCGCAACTCGCACTCCGATTAATATACGCCGCCAAC 2003
 Db 349 TTCAATTAATAGTCTGTTGCGCGGCGCAACTCGCACTCCGATTAATATACGCCGCCAAC 290
 Qy 2004 CGGCATTAAGAAATGGAAGAGAGTTTCACTGCATGCGAGATTCGTGATTTGATTCAG 2063
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 Qy 2064 CCCATATCGTTTCAATAGTCTTGCACCAACCGAACGACATTTGCAAGTACTCAGCGTAAGT 2123
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 Qy 2124 GATGTCACCTCGATATGTCATCTGTAAAGCAATTTTCCAGAGACGAGCGGTATCT 2183
 Db 169 GATGTCACCTCGATATGTCATCTGTAAAGCAATTTTCCAGAGACGAGCGGTATCT 110
 Qy 2184 CTTTCATAGGCTTAATGAGTCTCTCCACGCGGTCCATCTTCCAGGAGTAAATAGGCCG 2243
 Db 109 CTTTCATAGGCTTAATGAGTCTCTCCACGCGGTCCATCTTCCAGGAGTAAATAGGCCG 50
 Qy 2244 CGGCGCTTCTTATGTTTGGCGCTTCGCATGGAGC 2281
 Db 49 CGGCGCTTCTTATGTTTGGCGCTTCCATTTTAC 12

RESULT 5
 BZ672965/c 944 bp DNA linear GSS 05-FEB-2003
 LOCUS PUBGD25TD.ZM_0.6_1.0_KB Zea mays genomic clone ZMBRta047F02,
 DEFINITION genomic survey sequence.
 BZ672965
 ACCESSION BZ672965.1 GI:28221885
 VERSION GSS.
 KEYWORDS Zea mays
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 944)
 WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Bennettzen,J.
 TITLE Maize Genomics Consortium
 JOURNAL Unpublished (2003)
 COMMENT Contact: Cathy WhiteLaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteLaw@tigr.org
 Seq primer: TP
 Class: sheared ends.

FEATURES
 Source
 Location/Qualifiers
 1..944
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 Cot selected genomic DNA library"

ORIGIN

Query Match 30.8%; Score 852.8; DB 8; Length 944;
 Best Local Similarity 94.0%; Pred. No. 7.2e-164;
 Matches 887; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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QY 1062 CGGATGTTTACATTAACCGGACATATATAGAGCTCTCACACACAGTTGGCTTTTG 1121
DB 944 CGGATGTTTACATTAACCGGACATATATAGAGCTCTCACACATATATATGCTCTTG 885
QY 1122 ATTTAAGCCGACGCTTTCCCGGATCCAGATCCAAACCTTCGCTTCAAAAATGGAAC 1181
DB 884 ATTTAAGCCGACGCTTTCCCGGATCCAGATCCAAACCTTCGCTTCAAAAATGGAAC 825
QY 1182 AACTTTACCGACCGCCCGGTTTATCATCCCTCGGTTATCATAGATAGCTGATGT 1241
DB 824 AACTTTACCGACCGCCCGGTTTATCATCCCTCGGTTATCATAGATAGCTGATGT 765
QY 1242 AGTTTCAGTGAAGCCCATTCCTTCTGCTGATCCTGGCAATGGAACCTTGGCAACCGC 1301
DB 764 AGTTTCAGTGAAGCCCATTCCTTCTGCTGATCCTGGCAATGGAACCTTGGCAACCGC 705
QY 1302 TTCCCGGACTTCTTGTAGAGGAGGAGCCGACAGAGCAATTCGTTAAATTAGATAA 1361
DB 704 TTCCCGGACTTCTTGTAGAGGAGGAGCCGACAGAGCAATTCGTTAAATTAGATAA 645
QY 1362 ATCGATTTTGTCAATCAGAGTCTTTTGGGAAAGAGATAGGTTGGCACACGACG 1421
DB 644 ATCGATTTTGTCAATCAGAGTCTTTTGGGAAAGAGATAGGTTGGTACTAGCAA 585
QY 1422 CGGACTTTGAATTTGTATTCCTGGAAGGCTCTCCAAACAGCTCTTCTTCAATCTAA 1481
DB 584 CGGACTTTGAATTTGTATTCCTGGAAGGATCGTAAACAGCTCTTCTTCAATCTAA 525
QY 1482 CATTAAGAGACTGGAATCCATATCAATCAATATCCGAGTGTAGTAAACATTCGAAAC 1541
DB 524 CATTAAGAGACTGGAATCCATATCAATATCCGAGTGTAGTAAACATTCGAAAC 465
QY 1542 GTGATGAAATGGAACAACATTTAAATCGCAGTATCCGAAATGTTGATTCGCAAAAT 1601
DB 464 GTGATGAAATGGAACAACATTTAAATCGCAGTATCCGAAATGTTGATTCGCAAAAT 405
QY 1602 AGGATCTTGGCATGCGAGAAATCTCACGCGGAGATTTCTATGAGGACGACGACCTT 1661
DB 404 AGGATCTTGGCATGCGAGAAATCTCACGCGGAGATTTCTATGAGGAGGACGACCTT 345
QY 1662 AGGACAGCAGTATCCAGAGAGTTCATGATCAATGCAATTTGCTTGTCCCTATGAA 1721
DB 344 AGGTAACCCAGTATCCAGAGAGATTCATTAATGATGCAATTTGCTTGTCCAGATCAA 285
QY 1722 GGAATCTGGCAAAAATCGTATTCATTTAAACCGGAGTATGAGATGACGAAAGT 1781
DB 284 GGAATCTGGTAAATAATCGTATTCATTTAAACCGGAGTATGAGATGACGAAAGT 225
QY 1782 GTACATGACTGAAATCCCTGTGTAATCCGTTTGAATTCATGATTAATATTTTGGAT 1841
DB 224 GTACATGACTGAAATCCCTGTGTAATCCGTTTGAATTCATGATTAATATTTTGGAT 165
QY 1842 GATTTGGAAGCTTTTGTGACGTTCAAAATTTTGTGCAACCCCTTTTGGAAAGGAAAC 1901
DB 164 TATTTGTAATTTTGTGACGTTCAAAATTTTGTGCAACCCCTTTTGGAAAGGAAAC 105
QY 1902 CAGGTAAGCTGGGAAATGCGCATACTGTTGAGCAATTCAGTTCAATTAATATGTCGT 1961
DB 104 TACGTAAGCTGGGAAATGTTCAATCTGTTGAGCAATTCAGTTCAATTAATATGTCGT 45
QY 1962 CGGAGGCGCACTGCAATCCGATTAATTAACGGGCGCAACCG 2005
DB 44 CGGAGGCGCACTGCAATCCGATTAATTAACGGGCGCAACCG 1

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RESULT 6
 B2670418/c

LOCUS B2670418 902 bp DNA linear GSS 05-FEB-2003

DEFINITION PUBEN17TD ZM 0.6-1.0 KB Zea mays genomic clone ZMBETA037C10,
 genomic survey sequence.

ACCESSION B2670418
 VERSION B2670418.1 GI:28217807

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 902)

AUTHORS White, C.A., Quackenbush, J., Van Aken, S., Uteback, T.,
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J., and
 Benner, J.

TITLE Maize Genomes Consortium

JOURNAL Unpublished (2003).

COMMENT Contact: Cathy White

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: white@tigr.org

Seq primer: TP

Class: sheared ends.

location/Qualifiers

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Query Match 30.0%; Score 831.6; DB 8; Length 902;
 Best Local Similarity 95.1%; Pred. No. 1.6e-159;
 Matches 858; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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QY 1344 TTGCTGTAATTAATGTAATCGTATTTGTCATATCAGAGTCTTTTGGCAAGAGAGAA 1403
DB 902 TTGCTGTAATTAATGTAATCGTATTTGTCATATCAGAGTCTTTTGGCAAGAGAGAA 843
QY 1404 TTAGGTTGGCACGACGACGCACTTTGAATCTTTGTAATCTTGAAGCTCTCAGAAACG 1463
DB 842 TTAGGTTGGTACTAGCAACGCACTTTGAATTTGTAATCTTGAAGGATCGTAAACAG 783
QY 1464 CTCTTTTCAATCTATATATTAAGGACCTGGAATCCAGATATCAATTAATCCAGATGT 1523
DB 782 CTCTTTTCAATCTATATATTAAGGACCTGGAATCCAGATATCAATTAATCCAGATGT 723
QY 1524 AGTAAACATTCGCAAAACCGTATGTAATGGAACAACACTTAAATCGCAGTATCCGGAAT 1583
DB 722 AGTAAACATTCGCAAAACCGTATGTAATGGAACAACACTTAAATCGCAGTATCCGGAAT 663
QY 1584 GATTTGATTTGCCAAAATAGATCTCTGCAATCGGAAATCTTCAACGAGCGAGTTTATG 1643
DB 662 GATTTGATTTGCCAAAATAGATCTCTGCAATCGGAAATCTTCAACGAGCGAGTTTATG 603
QY 1644 AGGCAAGGACGACCTTTAGGAGACCAATATATCCAGAGGATTCATGATCAGTCAAT 1703
DB 602 CGGAAAGGCGACACCTTTAGGAGTAAACCAATATATCCAGAGGATTCATGATCAGTCAAT 543
QY 1704 TGTCTTGTCCCTATCGAAGGACTCTGGCAAAATGTAATTCATTTAAACCGGAGAGTAG 1763
DB 542 TGTCTTGTCCCTATCGAAGGACTCTGGTACAAATGTAATTCATTTAAACCGGAGAGTAG 483
QY 1764 ATGAGATGTGACGACGCTGATCATGAGTGAATCCCTGTAATCCGTTTGAATTCAT 1823
DB 482 ATGAGATGTGACGACGCTGATCATGAGTGAATCCCTGTAATCCGTTTGAATTCAT 423

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QY 1824 GATATATATTTTGGATGATGGAGCTTTTGGACGTTCAAAATTTTGGACCC 1883
 Db 422 GATATATATTTTGGATGATGGAGCTTTTGGACGTTCAAAATTTTGGACCC 363
 QY 1884 CTTTGGAAAACGAAACACGAGTAGGCTGGAAATGCCATCTCTGGAGAAATTCACG 1943
 Db 362 CTTTGGAAAACGAAACACGAGTAGGCTGGAAATGCCATCTCTGGAGAAATTCACG 303
 QY 1944 TTCAATTAATATGTCGTCGGGGGCGCAACTGCACTCCGATTAATTAACGCCCCACAC 2003
 Db 302 TTCAATTAATATGTCGTCGGGGGCGCAACTGCACTCCGATTAATTAACGCCCCACAC 243
 QY 2004 CGGCAATTAAGAAATTAAGAGAGTTTTCATCTGATTCGAGCAATTCGATTTGATTCAG 2063
 Db 242 CGGCAATTAAGAAATTAAGAGAGTTTTCATCTGATTCGAGCAATTCGATTTGATTCAG 183
 QY 2064 CCATATGCTTTCATGCTTCGCGCAACGGAAGGAGATTCGAGTTCGAGTTCAGT 2123
 Db 182 CCATATGCTTTCATGCTTCGCGCAACGGAAGGAGATTCGAGTTCGAGTTCAGT 123
 QY 2124 GATGTCACCTCGATATGTCATCTGTAAAGCAATTTGTCAGGACGAGGCTATCT 2183
 Db 122 GATGTCACCTCGATATGTCATCTGTAAAGCAATTTGTCAGGACGAGGCTATCT 63
 QY 2184 CTTGATAGCTTATGCACTGCTCTCCAGCGGTTCCATCTTCCAGCGAGTGAATGCGC 2243
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 QY 2244 CG 2245
 Db 2 CG 1

RESULT 7
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 LOCUS B2678861
 DEFINITION PUBX85TD ZM_0.6_1.0_KB Zea mays genomic clone ZM5BTA043K17,
 genomic survey sequence.
 ACCESSION B2678861
 VERSION B2678861.1 GI:28232442
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 929)
 WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Resnick,A., Frazer,C.W., Yuan,Y., San Miguel,P., Ma,J. and
 Benneker,J.
 Maize Genomics Consortium
 Unpublished (2003)
 Contact: Cathy Whitelaw
 TIGR
 912 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TP
 Class: sheared ends.

FEATURES
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Best Local Similarity 93.9%; Pred. No. 1,1e-158;
 Matches 872; Conservative 0; Mismatches 56; Indels 1; Gaps 1;
 QY 747 TTTGGCGGTGTACTTGAACCTGCGAGCAATTCACGATCTCTTTTCCGTATGCTCTT 806
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 QY 866 CTGCGACACCTGCGTCGAAAGATGTTGGGGTGTGGAGCAAGATGATTCGAATTCAGCGG 925
 Db 121 CTGCGACGCGCGCTCGAAGATGTTGGGGTGTGTAACAATTCATTCGAATTCAGCGG 180
 QY 926 GAGCGACCTGATTAACCTTTGACTTAATCAGAGCTTCAGCGGCTCAACGATGAAGAACT 985
 Db 181 GAGCGACCTGATTAACCTTTGACTTAATTAAGCTTCAGCGGCTCAACGATGAAGAACT 240
 QY 986 GTTGTGCTGCTCCAGTAAGCTATGCTCTCAGAAATGAGCAATCCATCCCTGTGCAATCA 1045
 Db 241 GTTGTGCTGCTCCAGTAAGCTATGCTCTCAGAAATGAGCAATCCATCCCTGTGCAATCA 300
 QY 1046 AGGCGTTGTCGCTTCCGGAATGTTTACATTAACCGGACATTAATCATAGACCTCTCACAC 1105
 Db 301 AGGCGTTGTCGCTTCCGGAATGTTTACATTAACCGGACATTAATCATAGACCTCTCACAC 360
 QY 1106 ACAGTTGCGCTCTTGAATTAACGCCGCTTTTCCGGTATCAGATTCACAACTCTCG 1165
 Db 361 ATAAATTCGCTCTGATTAACGCCGCTTTTCCGGTATCAGATTCACAACTCTCG 420
 QY 1166 CTTCAAAAAATGGAACAACCTTACCCGACGCGCGCGGTTATATATCCCGCTGGGTGTA 1225
 Db 421 CTTCAAAAAATGGAACAACCTTACCCGACGCGCGCGGTTATATATCCCGCTGGGTGTA 480
 QY 1226 TCAGAAATAGCTGATGATGTCATGTCAGTGAAGCCATATCTTTCCTGATATCTGCGAGATGGA 1285
 Db 481 TCAGAAATAGCTGATGATGTCATGTCAGTGAAGCCATATCTTTCCTGATATCTGCGAGATGGA 540
 QY 1286 ACCTCTTGGCAACCGCTTCCCGCACTTCTTAAGAGGGGAGGCCACCAAGCAATTT 1345
 Db 541 AGCGTTTGGCAACCGCTTCCCGCACTTCTTAAGAGGGGAGGCCACCAAGCAATTT 600
 QY 1346 CGTGAATATAGATTAATCGTATTTGTCATCGAGAGCTTTGGGAGAGAGAGATA 1405
 Db 601 CGTGAATATAGATTAATCGTATTTGTCATCGAGAGCTTTGGGAGAGAGATA 660
 QY 1406 GGGTTGGCACACGACGACGCACTTGAATCTTGTATCTTGAAGGCTCTCAGAAACAGCT 1465
 Db 661 GGGTTGGCACACGACGACGCACTTGAATCTTGTATCTTGAAGGATCGTAAACAGCT 720
 QY 1466 CTTCTTCAATCTATATCATTTAAGACGATCGAAATCCATATCAATTCGAGGTGAG 1525
 Db 721 CTTCTTCAATCTATATCATTTAAGACGATCGAAATCCATATCAATTCGAGGTGAG 780
 QY 1526 TAAACATTCCAAAACCGTATGATGATGAAGCAACACTTAAATTCGAGATTCGAGATGA 1585
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 QY 1586 TTTGATTCGCAAAAATAGATCTTGGCATTCGCAAGATTCACGCAAGCATTTCTATGAG 1645
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 QY 1646 GCGAGCGCACCTTATGAGCAACCGGTA 1674
 Db 901 GAAAGGCGCACACCCCTAGTAACCCAGTA 929

RESULT 8
 B2671975 911 bp DNA linear GSS 05-FEB-2003
 LOCUS B2671975
 DEFINITION PUBX85TD ZM_0.6_1.0_KB Zea mays genomic clone ZM5BTA039P02,
 genomic survey sequence.

ACCESSION B2671975
 VERSION B2671975.1 GI:28220321
 KEYWORDS CSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 911)
 WhiteIaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Bennettzen,J.
 Maize Genomics Consortium
 Unpublished (2003)
 COMMENT Contact: Cathy WhiteIaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteIaw@tigr.org
 Seq primer: TF
 Class: sheared ends.
 Location/Qualifiers
 1..911
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_1b="ZMMB7a039P02"
 /note="Vector: pCR4-TOBO; Site_1: EcoRI; 0.6-1.0 kb high
 cot selected genomic DNA library"

ORIGIN

Query Match 29.3%; Score 811.8; DB 8; Length 911;
 Best Local Similarity 93.2%; Pred. No. 1.8e-155;
 Matches 849; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 845 CGGCGTCATCGTCGGGAGACCTGCGACACCTGCGTGAAGATGTTGGGGTGTGAGCA 904
 DB 1 CGGCGTCATCGTCGGGAGACCTGCGACACCTGCGTGAAGATGTTGGGGTGTGAGCA 60
 QY 905 AGATGATTCATTCAGCGGGAGCCACTGATAGCTTTGTACTTAATAGACTTCA 964
 DB 61 ATATCATTCATTCAGCGGGAGCCACTGATAGCTTTGTACTTAATAGACTTCA 120
 QY 965 GGGGTCACAGAGAGAGAGTGTTCGCTTCGTCGCCAGTAGCTCTCCAGATGTA 1024
 DB 121 AGGGGTCACTAGAGAGAGTGTTCGCTTCGTCGCCAGTAGCTCTCCAGATGTA 180
 QY 1025 GCCATCCATCTTGTCAATCAAGGCGTGTGCTTCGATTCGATTAACCGGACA 1084
 DB 181 GCCATCCATCTTGTCAATCAAGGCGTGTGCTTCGATTCGATTAACCGGACA 240
 QY 1085 TAATCATGAGACTCTCAACACAGTTGCGCTCTTTGATTAAGCCCGAGTTTCCCG 1144
 DB 241 TAATCATGAGACTCTCTGACACATTAATTCGCTCTCTGATTAAGCCCGAGTTTCCCG 300
 QY 1145 TATCCGATCCACACCTTGGCTCAAAAATGGAACAACCTTAACGACGCGCGCGGT 1204
 DB 301 TATCCGATCCACACCTTGGCTCAAAAATGGAACAACCTTAACGACGCGCGCGGT 360
 QY 1205 TATCATCCCTCGGGTGTATCAGAAATAGCTGATAGTCTCAGTAGGCCATATCTT 1264
 DB 361 TATCATCCCTCGGGTGTATCAGAAATAGCTGATAGTCTCAGTAGGCCATATCTT 420
 QY 1265 GCGTGAATCTGGCAGATGGAACCTTTGGCAACCGCTTCCCGAGCTTCTTGAAGAGG 1324
 DB 421 GCGTGAATCTGGCAGATGGAAGCTTTTGGCAACCGCTTCCCGAGCTTCTTGAAGAG 480
 QY 1325 GAGGCGACACAGAAATTTGCTGAATTAATGATTAATGATTTGTCATCAGATGTC 1384
 DB 481 GTGGGCCCCGAGAGCAATTCGTGAATTAATGATTAATGATTTGTCATCAGATGTC 540

QY 1385 TTTGGCGAAGAGAGAAATAGGTTGCGACGACCGCACTTGAATCTGTAAATCCT 1444
 DB 541 TTTGGCGAAGAGAGAAATAGGTTGCTGACTAGCAACCGCACTTGAATCTGTAAATCCT 600
 QY 1445 GAAGGCTCTCGCAAAACAGCTCTTCTCAATCTATATCATTAAGACGACTGAAATCCAC 1504
 DB 601 GAAGGATGTGAATAAACAGCTCTTCTCAATCTATATCATTAAGACGACTGAAATCCAC 660
 QY 1505 ATATCAATATTCGAGTGTATGTAACATTCGAAACCGGATGGAATGGAACAACCTTA 1564
 DB 661 ATATCAATATTCGAGTGTATGTAACATTCGAAACCGGATGGAATGGAACAACCTTA 720
 QY 1565 AATGCGAGATCCGGAATGATTTGATGCCAAAATAGATCTGCGATGCGAGAAATC 1624
 DB 721 AATGCGAGATCCGGAATGATTTGATGCCAAAATAGATCTGCGATGCGAGAAATC 780
 QY 1625 TCACGAGGACAGTTCTATGAGGAGAGACACCTTTAGGACAGACGATAGATCCAGAG 1684
 DB 781 TCACGAGGACAGTTCTATGCGGAGGAGGACACCTTTAGGTAACGATAGATCCAGAG 840
 QY 1685 AGTTCAATATCAGTGAATTTGCTTCTTATCGAAGACTCTGCGACAAAATCGTATT 1744
 DB 841 AATTCAATATCAGTGAATTTGCTTCTTATCGAAGACTCTGCGACAAAATCGTATT 900
 QY 1745 CATTAAACCG 1755
 DB 901 CATTAAACCG 911

RESULT 9
 B2686758 885 bp DNA linear GSS 05-FEB-2003
 LOCUS PUBF30TD_ZM_0.6.1.0_KB Zea mays genomic clone ZMMB7a041F11,
 DEFINITION genomic survey sequence.
 ACCESSION B2686758
 VERSION B2686758.1 GI:28247291
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 885)
 WhiteIaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Bennettzen,J.
 Maize Genomics Consortium
 Unpublished (2003)
 COMMENT Contact: Cathy WhiteIaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteIaw@tigr.org
 Seq primer: TF
 Class: sheared ends.
 Location/Qualifiers
 1..885
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_1b="ZMMB7a041F11"
 /note="Vector: pCR4-TOBO; Site_1: EcoRI; 0.6-1.0 kb high
 cot selected genomic DNA library"

ORIGIN

Query Match 29.2%; Score 809.8; DB 8; Length 885;
 Best Local Similarity 94.7%; Pred. No. 4.5e-155;
 Matches 838; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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QY 695 CCGTAAGACCTTTGGGATCTTGTGTCACAAACAACTCTTCGGCAACTTTTTCGGCG 754
Db 1 CCGTAAGACCTTTGGGATCTTGTGTCACAAACAACTCTTCGGCAACTTTTTCGGCG 60
QY 755 TTGTACTGACTGGCGAGTAATCCAGATCTTTTTCGGTATCGTCTTTCGGTCT 814
Db 61 TTGTACTGACTGGCGAGTAATCCAGATCTTTTTCGGTATCGTCTTTCGGTCT 120
QY 815 CCAAAACAACAACGCGCGGGAAGTTACCGCGCTCATCGTGGGAAGACCTGGCAAC 874
Db 121 CCAAAACAACAACGCGCGGGAAGTTACCGCGCTCATCGTGGGAAGACCTGGCAAC 180
QY 875 CTGCGTCGAAGATGTTGGGAGTGTGGAGCAAGATGGAATTCGAATTCAGCGGAGCCACT 934
Db 181 CCGCGTCGAAGATGTTGGGAGTGTGGAGCAAGATGGAATTCGAATTCAGCGGAGCCACT 240
QY 935 GATGACCTTTGACTTAATCAGAGCTTCAGCGGTCAGCAATGGAAGAGTTCGTCTT 994
Db 241 GATGACCTTTGACTTAATCAGAGCTTCAGCGGTCAGCAATGGAAGAGTTCGTCTT 300
QY 995 CGTCCAGTAAGCTATGTCCTCAGAGATGAGCAATCCATCCCTTGTCAATCAAGCGTTGG 1054
Db 301 CGTCCAGTAAGCTATGTCCTCAGAGATGAGCAATCCATCCCTTGTCAATCAAGCGTTGG 360
QY 1055 TCGCTTCGGAATGTTTACATTAACCGGACATTAATCATAAGACCTTCACACAGTTCCG 1114
Db 361 TCGCTTCGGAATGTTTACATTAACCGGACATTAATCATAAGACCTTCACACAGTTCCG 420
QY 1115 CTCTTTGATTAAACCGCCAGCTTTTTCGGGTATCCAGATCCAACTTCGCTTCAAAA 1174
Db 421 CTCTTTGATTAAACCGCCAGCTTTTTCGGGTATCCAGATCCAACTTCGCTTCAAAA 480
QY 1175 ATGGAACAACCTTACCGGACCGCGCGGTTATATCCCGCTCGGGGTATACAGAAATAG 1234
Db 481 ATGGAACAACCTTACCGGACCGCGCGGTTATATCCCGCTCGGGGTATACAGAAATAG 540
QY 1235 CTGATGATGCTCAGTGAAGCCCATATCTTTCCTGATACCTGGCAGATGGAACCTCTTGG 1294
Db 541 CTGATGATGCTCAGTGAAGCCCATATCTTTCCTGATACCTGGCAGATGGAACCTCTTGG 600
QY 1295 CAACCGGCTCCCGGACTTCTTACAGAGGGAGCGCCACCGAAGCAATTTCTGTAAAT 1354
Db 601 CAACCGGCTCCCGGACTTCTTACAGAGGGAGCGCCACCGAAGCAATTTCTGTAAAT 660
QY 1355 TAGATAATGATTTGTCAATCAGATGCTTTTGGGAGAGAGAAATAGGGTGGCA 1414
Db 661 TAGATAATGATTTGTCAATCAGATGCTTTTGGGAGAGAGAAATAGGGTGGCA 720
QY 1415 CAGCAGCGCACTTTGAATCTTGAATCTGGAAGCTCTCAGAAACAGCTCTTCTCAA 1474
Db 721 CAGCAGCGCACTTTGAATCTTGAATCTGGAAGCTCTCAGAAACAGCTCTTCTCAA 780
QY 1475 ATCTATCATTAAGACGCTCGAAATCCACATATCAATATCCAGTGTAGTAAACATTC 1534
Db 781 ATCTATCATTAAGACGCTCGAAATCCACATATCAATATCCAGTGTAGTAAACATTC 840
QY 1535 CAAAACCGTATGGAATGGAACAACCTTAAATCGAGTATCCG 1579
Db 841 CAAAACCGTATGGAATGGAACAACCTTAAATCGAGTATCCG 885

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```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.
FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="873"
/db_xref="takon:4577"
/clone="ZMBRta083A13"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"
ORIGIN
Query Match 29.0%; Score 804.8; DB 8; Length 884;
Best Local Similarity 94.7%; Pred. No. 4.8e-154;
Matches 833; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 700 AGACCTTGGGTACTTCGTGTCACAAACAACTCTTCGGGCAACTTTTTCGGGTTGT 759
Db 5 AGACCTTGGGTACTTCGTGTCACAAACAACTCTTCGGGCAACTTTTTCGGGTTGT 64
QY 760 ACTGATGCGCAGATATCAGATCTCTTTTCGTATCGTCTTCCGTCCAAA 819
Db 65 ACTGATGCGCAGATATCAGATCTCTTTTCGTATCGTCTTCCGTCCAAA 124
QY 820 ACAACAACGCGCGGGAAGTTACCGCGCTCATCGTGGGAAGACCTGGACACCTCG 879
Db 125 ACAACAACGCGCGGGAAGTTACCGCGCTCATCGTGGGAAGACCTGGACACCTCG 184
QY 880 TCGAAGATGTTGGGGTGTGGAGCAAGATGGAATTCGAATTCAGCGGAGCCACTGATAG 939
Db 185 TCGAAGATGTTGGGGTGTGGAGCAAGATGGAATTCGAATTCAGCGGAGCCACTGATAG 244
QY 940 CTTTGTACTTAATCAGAGACTTCAGGCGGTCAAGATGGAAGAGTTCGTCTGTC 999
Db 245 CTTTGTACTTAATCAGAGACTTCAGGCGGTCAAGATGGAAGAGTTCGTCTGTC 304
QY 1000 CAGTAAGCTATGCTCCAGATGAGCCATTCATCTTGTCAATCAAGCGTTGTGCT 1059
Db 305 CAGTAAGCTATGCTCCAGATGAGCCATTCATCTTGTCAATCAAGCGTTGTGCT 364
QY 1060 TCGGATGTTTTCATTAACCGGACATATCATAGACCTCTCACAACAGTTGCTCTT 1119
Db 365 TCGGATGTTTTCATTAACCGGACATATCATAGACCTCTCTGACATATTCGCTCTC 424
QY 1120 TGAATACGCCGAGCTTTTTCGGGTATCCAGATCCCAACCTTGCTCAAAAATGGA 1179
Db 425 TGAATACGCCGAGCTTTTTCGGGTATCCAGATCCCAACCTTGCTCAAAAATGGA 484
QY 1180 ACAACTTTCACGACCGCGCGGTTATATCATCCCTCGGGTGTATCAGAAATAGCTGAT 1239
Db 485 ACAACTTTCACGACCGCGCGGTTATATCATCCCTCGGGTGTATCAGAAATAGCTGAT 544
QY 1240 GTAAGTCTGATGAGCCATATCTTTCGTGATACCTGCGAGATGGAACCTCTTGCAAC 1299
Db 545 GTAAGTCTGATGAGCCATATCTTTCGTGATACCTGCGAGATGGAAGCTCTTGCAAC 604
QY 1300 GCTTCCCGCACTTCTTACAGAGGGAGCGCACCAAGAACTTTCGTTAAATTAAGAT 1359

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RESULT 10
LOCUS
BZ703458 884 bp DNA linear GSS 19-FEB-2003
DEFINITION
PUB007772 ZM_0.6_1.0_KB Zea mays genomic clone ZMBRta083A13,
genomic survey sequence.
ACCESSION
BZ703458
VERSION
BZ703458.1 GI:28423866
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD

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Db 605 GCTTCCCGACTCTTTCGAAAGAGGTGGCCGCCGAAAGCAATTCGTGTAATTAGAT 664

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Db 665 AATATGTAATTTGTCATCAGAGTCTTTTGGCGAAAGAGTAATGGTTGGTACTTAC 724

Qy 1420 AGCGACTTGAATCTTGTAACTCTTGAAGGCTCTCAGAAACAGCTCTTCTTAATCTA 1479

Db 725 AACGACTTTGAATTTTGTATCTCTGAAGGATCTGTAAGAACGCTCTTCTTAATCTA 784

Qy 1480 TACATTAGACGACTCGAAATCCATATCAATATCCAGTGTAGTAATAACATTCGAAA 1539

Db 785 TACATTAGACGACTCGAAATCCATATCAATATCCAGTGTAGTAATAACATTCGAAA 844

Qy 1540 CCCTGATGGAATGGAACACACTTAAATATGCGAGTTCGG 1579

Db 845 CCGTATGGAATGGAACACACTTAAATATGCGAGTTCGG 884

RESULT 11

BZ679896/c 916 bp DNA linear GSS 05-FRB-2003

LOCUS PUBEVL3TD.ZM.0.6.1.0.KB.Zea.mays.genomic.clone.ZM87A039C02,

DEFINITION genomic survey sequence.

ACCESSION BZ679896

VERSION BZ679896.1 GI:28234344

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 916)

WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennettzen,J.

Maize Genomics Consortium

Unpublished (2003)

CONTACT: Cathy WhiteJaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitejaw@tigr.org

Seq primer: TF

Classes: sheared ends.

FEATURES

Location/Qualifiers

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/strain="B73"

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/note="Vector: PCR4-T0B0; Site 1: EcorI; 0.6-1.0 kb high cot selected genomic DNA library"

ORIGIN

Query Match 29.0%; Score 803.4; DB 8; Length 916;

Best Local Similarity 93.2%; Pred. No. 9.3e-154;

Matches 851; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

Qy 1026 CCATCAATCTTGTCAATCAAGGCGTTGCTTCGCGATTGTTTACATACCGGACAT 1085

Db 916 CCATCAATCTTGTCAATCAAGGCGTTGCTTCGCGATTGTTTACATACCGGACAT 857

Qy 1086 AATCATAGGACCTCTGACACAGCTTCGCTCTTGTATTAAGCCGCGATTTCCGGGT 1145

Db 856 AATCATAGGACCTCTGACACATATTCGCTCTTGTATTAAGCCGCGATTTCCGGGT 797

Qy 1146 ATCCAGATCCACACCTTCGCTTCAAAAAATGGAACAATTTCAGACCGCGCGGTTT 1205

Db 796 ATCCAGATCCACACCTTCGCTTCAAAAAATGGAACAATTTCAGACCGCGCGGTTT 737

Qy 1206 ATCATCCCTCGGCGGTATCAGATAGCTAGTCTGAGAGCCATATCTTG 1265

Db 736 ATCATCCCTCGGCGGTATCAGATAGCTAGTCTGAGAGCCATATCTTG 677

Qy 1266 CCTGATACCTGACAGATGGAACTCTTGGCAACGCTTCCGACTTCTTGAAGAGGG 1325

Db 676 TCGTATCCCTGGAAGATGGAACTTTCGCAACCGCTTCCGACTTCTTGAAGAGGG 617

Qy 1326 AGCGCACAGAGCAATTTCTGTATTAATTAATTAATTTGTGCAATCAGAGTGT 1385

Db 616 TCGCGCCCCAGAGCAATTTCTGTATTAATTAATTAATTTGTGCAATCAGAGTGT 557

Qy 1386 TTTGGGAAAGAGGAATAGGGTTGGACGACGACGACCTTGAATCTTGAATCTGT 1445

Db 556 TTTGGGAAAGAGGAATAGGGTTGGTCTGACGACGACCTTGAATCTTGAATCTGT 497

Qy 1446 AAGGCTCTCAGAAAACGCTCTTCTTCAATCTATACATTAAGACGACTCGAAATCCACA 1505

Db 496 AAGGATCGTAAAAAACGCTCTTCTTCAATCTATACATTAAGACGACTCGAAATCCACA 437

Qy 1506 TATCAATATCCGAGTGTATGTAACATTCGAAACCGTATGGAATGGAACAACTTAA 1565

Db 436 TATCAATATCCGAGTGTATGTAACATTCGAAACCGTATGGAATGGAACAACTTAA 377

Qy 1566 AATCGAGTATCCGGAATGATTTGATTTGACCAAAAATAGGATCTTGGCATGCGAAGATCT 1625

Db 376 AATCGAGTATCCGGAATGATTTGATTTGACCAAAAATAGGATCTTGGCATGCGAAGATCT 317

Qy 1626 CACGACGAGCTTATATGAGGACGACGACACCTTTAGGACAGCATAGATCCAGAGGA 1685

Db 316 GACGACGAGCTTATATGAGGACGACGACACCTTTAGGTAACCGATGATCCAGAGGA 257

Qy 1686 GTTCATGATCAGTGCATTTGCTTGTCTTCTTATGCAAGGACTTGGCAAAAATCGATTTC 1745

Db 256 ATTCAATATCAGTGCATTTGCTTGTCTTCTTATGCAAGGACTTGGTACAAAATCGATTTC 197

Qy 1746 ATTAAACCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1805

Db 196 ATTAAACCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 137

Qy 1806 ATCCGTTTGAATCCATGATATATATTTTGTGATGATGATGATGATGATGATGATGAT 1865

Db 136 ATCCGTTTGAATCCATGATATATATTTTCTGATATATTTTGTGATGATGATGATGAT 77

Qy 1866 CAAATTTTTCGCAACCTTTTGGAAACGACACGATGATGATGATGATGATGATGAT 1925

Db 76 CAAATTTTTCGCAACCTTTTGGAAACGACACGATGATGATGATGATGATGATGAT 18

Qy 1926 ACTGTGAGCAAT 1938

Db 17 ACTGTGAGCAAT 5

RESULT 12

BZ682015/c 866 bp DNA linear GSS 05-FRB-2003

LOCUS PUBJP02TD.ZM.0.6.1.0.KB.Zea.mays.genomic.clone.ZM87A070A04,

DEFINITION genomic survey sequence.

ACCESSION BZ682015

VERSION BZ682015.1 GI:28237996

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 866)

WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennettzen,J.

Maize Genomics Consortium

Unpublished (2003)

JOURNAL

| | | | |
|----|------|--|------|
| Db | 652 | CCTTAGTAAACCCAGTAGATCCAGAGAAATTCATTATCAGTCAATTTGTCACGAT | 593 |
| Qy | 1718 | CGAAGACTCTGCGCAAAAATGTATTCATTTAAACCGGAGAGTGAAGATGTCAGCA | 1777 |
| Db | 592 | CMAAGACTCTGCGCAAAAATGTATTCATTTAAACCGGAGAGTGAAGATGTCAGCA | 533 |
| Qy | 1778 | ACGTGTACATCGACTGAAATCCCTGTAAATCCGTTTGAATTCATGATTAATATTTT | 1837 |
| Db | 532 | ACGTGTACATCGACTGAAATCCCTGTAAATCCGTTTGAATTCATGATTAATATTTT | 473 |
| Qy | 1838 | GGATGATTTGGAGGCTTTTTCACGCTTCAAAAATTTTTCGAAACCCCTTTTGGAAACA | 1897 |
| Db | 412 | GGATGATTTGGAGGCTTTTTCACGCTTCAAAAATTTTTCGAAACCCCTTTTGGAAACA | 413 |
| Qy | 1898 | ACACACGCTAGGCTGCGAAATGCCATTCCTTTGAGCAATTCAGTTTCATTAATAT | 1957 |
| Db | 412 | ACACACGCTAGGCTGCGAAATGCCATTCCTTTGAGCAATTCAGTTTCATTAATAT | 353 |
| Qy | 1958 | CGTTGCGGGGCGCACTGCAATCCGATTAATACGCGCCCAACACCGGCAATTAAGAAAT | 2017 |
| Db | 352 | CGTTGCGGGGCGCACTGCAATCCGATTAATACGCGCCCAACACCGGCAATTAAGAAAT | 293 |
| Qy | 2018 | GAAGAAGTTTCTACTGCAATGACGATTCGTGATTTGTATTCAGCCCATATCGTTCA | 2077 |
| Db | 292 | GAAGAAGTTTCTACTGCAATGACGATTCGTGATTTGTATTCAGCCCATATCGTTCA | 233 |
| Qy | 2078 | TAGCTTTCGCCAACCGAAGGATTTGCAAGTACTCAGCGTAACTGATGTCACCTCGA | 2137 |
| Db | 232 | TAGCTTTCGCCAACCGAAGGATTTGCAAGTACTCAGCGTAACTGATGTCACCTCGA | 173 |
| Qy | 2138 | TATGTCATCTGTAAAGCAATTTGTCAGAAACGAGGCGTATCTTTCATAGCCTTAT | 2197 |
| Db | 112 | TATGTCATCTGTAAAGCAATTTGTCAGAAACGAGGCGTATCTTTCATAGCCTTAT | 113 |
| Qy | 2198 | GCAAGTGTCTTCACGCGGTTCCATCTTCCAGCGGATAGATGCGCGGCGCTTTCTT | 2257 |
| Db | 112 | GCAAGTGTCTTCACGCGGTTCCATCTTCCAGCGGATAGATGCGCGGCGCTTTCTT | 53 |
| Qy | 2258 | TGTTTGGCGCTTTCATGAGAC | 2281 |
| Db | 52 | TGTTTGGCGCTTTCATGAGAC | 29 |

RESULT 14
 BZ682835 882 bp DNA linear GSS 05-FEB-2003
 LOCUS PUBP67TD ZM.0.6.1.0 KB Zea mays genomic clone ZMMBTa050L14,
 DEFINITION genomic survey sequence.
 ACCESSION BZ682835
 VERSION BZ682835.1 GI:28239565
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 882)
 White, A., Quackenbush, J., Van Aken, S., Uterback, T.,
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
 Benzer, J.
 Maize Genomics Consortium
 Unpublished (2003)
 CONTACT Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: 1P
 Clones: sheared ends.
 Location/Qualifiers
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 /organism="Zea mays"

| | | | |
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| Db | 5 | AGACCTTTCGGTACTGCTCCACAAACGCAATCTCCCGGCAACTTTTTCGGGTTGTT | 64 |
| Qy | 760 | ACTGACTGCGGACGTAAATCCAGATCTCTTTTCCGTCATCGTCTTTCGGTCCAAA | 819 |
| Db | 65 | ACTGACTGCGGACGTAAATCCAGATCTCTTTTCCGTCATCGTCTTTCGGTCCAAA | 124 |
| Qy | 820 | ACAACACGCGCGCGGAAAGTTCAACCGGCTCATGTGTGGGAAAGCTGCGACACTCGC | 879 |
| Db | 125 | ACAACACGCGCGCGGAAAGTTCAACCGGCTCATGTGTGGGAAAGCTGCGACACTCGC | 184 |
| Qy | 880 | TGGAAGATGTTGGGTTGGAAGCAAGATGATTCATTCATTCAGCGGGAACCTGATAG | 939 |
| Db | 185 | TGGAAGATGTTGGGTTGGAAGCAAGATGATTCATTCATTCAGCGGGAACCTGATAG | 244 |
| Qy | 940 | CCTTTGACTTAATCAGACCTTCAGCGGCTCAACGATGAAGATGTTGTTGTTGCTTC | 999 |
| Db | 245 | CCTTTGACTTAATCAGACCTTCAGCGGCTCAACGATGAAGATGTTGTTGTTGCTTC | 304 |
| Qy | 1000 | CAGTAAGTATGTCTCCAAATGTAAGCATTCATCTTGTCAATGAAGCGTTGCTGCT | 1059 |
| Db | 305 | CAGTAAGTATGTCTCCAAATGTAAGCATTCATCTTGTCAATGAAGCGTTGCTGCT | 364 |
| Qy | 1060 | TCCGATGTTGTTTACCAACCGGACATTAATCAATGAGGCTTCACACAGATTTGCTCTT | 1119 |
| Db | 365 | TCCGATGTTGTTTACCAACCGGACATTAATCAATGAGGCTTCACACAGATTTGCTCTT | 424 |
| Qy | 1120 | TGATTAAGCGCCAGGCTTTTCCCGGTATCCAGATCCAAACCTTGCCTCAAAAATGGA | 1179 |
| Db | 425 | TGATTAAGCGCCAGGCTTTTCCCGGTATCCAGATCCAAACCTTGCCTCAAAAATGGA | 484 |
| Qy | 1180 | ACAACCTTACCGACCGCGCGGTTTATCATCTCCCTCGGTTGATATCAATAGCTGAT | 1239 |
| Db | 485 | ACAACCTTACCGACCGCGCGGTTTATCATCTCCCTCGGTTGATATCAATAGCTGAT | 544 |
| Qy | 1240 | GTAAGTCAGAGAGCGGCAATCTTCCCTGATACCTGCGACATGGAACCTTGGCAACC | 1299 |
| Db | 545 | GTAAGTCAGAGAGCGGCAATCTTCCCTGATACCTGCGACATGGAACCTTGGCAACC | 604 |
| Qy | 1300 | GCTTCCCGGACTTCTTGAAGAGGAGCGCACAGAAAGCAATTTCTGTAAATTAAGAT | 1359 |
| Db | 605 | GCTTCCCGGACTTCTTGAAGAGGAGCGCACAGAAAGCAATTTCTGTAAATTAAGAT | 664 |
| Qy | 1360 | AAATGTAATTTGTCAATCAGAGTCTTTTGGCGAAGAGAGATAGGTTGGACCAAC | 1419 |
| Db | 665 | AAATGTAATTTGTCAATCAGAGTCTTTTGGCGAAGAGAGATAGGTTGGACCAAC | 724 |
| Qy | 1420 | AGCGCACTTGAATTTGTAATCTGGAAGGCTCTTCAGAAACAGCTCTTTCGAATCTA | 1479 |
| Db | 725 | AGCGCACTTGAATTTGTAATCTGGAAGGAGATGTAACAGCTCTTTCGAATCTA | 784 |
| Qy | 1480 | TACATTAGACGACTCGAAATCCACATATCAATATCCAGTGTAGTAACATTCGAAAA | 1539 |
| Db | 785 | TACATTAGACGACTCGAAATCCACATATCAATATCCAGTGTAGTAACATTCGAAAA | 844 |
| Qy | 1540 | CCGTGATGAAATGGAACCAACTTAATTCGAGTATCC | 1578 |
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/mol type="genomic DNA"
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Query Match 28.6%; Score 793.4; DB 8; Length 882;
 Best Local Similarity 94.7%; Pred. No. 1e-151;
 Matches 832; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

RESULT 15
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 LOCUS
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 genomic survey sequence.
 accession BZ683904
 version BZ683904.1 GI:28241625
 keywords GSS.
 source Zea mays
 organism Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 867)
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
 Benneken, J.
 TITLE Maize Genomics Consortium
 JOURNAL Unpublished (2003)
 COMMENT Contact: Cathy Whitelaw
 TIGR
 912 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TF
 Class: sheared ends.
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 location/Qualifiers
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 Best Local Similarity 95.4%; Pred. No. 1.6e-150;
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 DB 807 AGACGACTCGAAATCCACATATCAAAATATCCAGGTAGTAAACATTCAGAAACCGTGAT 748
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 DB 687 CTCGGCATCGAGAAATCTCAGCAGGCACTTCTATGCGAAGGCAACCTTAGGTA 628
 QY 1667 GACCAGTAGATCCAGAGAGATTCATATCAGTGCAATTTGTCTTCTTATCGAAGAGCT 1726
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 QY 1727 CTGGCAGCAAAATGTATTTAAACCGGAGGTAGATGATGACGAACTGTACA 1786
 DB 567 CTGGTACAAATGTATTTAAACCGGAGGTAGATGATGACGAACTGTACA 508
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 DB 507 TCGACTGAATTCCTGTGTATCGTTTGAATCCATGATTAATTTTCTGATTAATG 448
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DB 447 GTAAATTTTTCACAGTTCAAAATTTTTCGAACCCCTTTTGGAAACAAACACTACG 388
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 QY 2207 CTCACCGGTTCCATCTTCCAGCGATAGATGCGCGGCTTTCTTATGTTTGG 2266
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 DB 27 CGCTTCCAT 18

Search completed: September 29, 2005, 17:34:28
 Job time : 8771 secs

[illegible]

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| Dp | 1441 | TCCTGAAGGCTCTCTCAGAAACGCTCTTCTTCAATCTATATCACTTAAAGCAGCTTCGAAT | 1500 |
| Qy | 1501 | CCACATATCATATATTCGAGTGTAGTAAACAATCCAAACCGTGATGSAATGSAACA | 1560 |
| Dp | 1501 | CCACATATCAATATTCGAGTGTAGTAAACAATCCAAACCGTGATGSAATGSAACA | 1560 |
| Qy | 1561 | CTTAAATTCGAGTATCCGGAATGATTTGATTCGCAAAAATAGATCTCTGGCATGCGAG | 1620 |
| Dp | 1561 | CTTAAATTCGAGTATCCGGAATGATTTGATTCGCAAAAATAGATCTCTGGCATGCGAG | 1620 |
| Qy | 1621 | AATCTCAGCGAGGAGCTTCTATGAGGAGACGACACCTTTAAGCAGACCAAGTATGATCCA | 1680 |
| Dp | 1621 | AATCTCAGCGAGGAGCTTCTATGAGGAGACGACACCTTTAAGCAGACCAAGTATGATCCA | 1680 |
| Qy | 1681 | GAGGAGTTCATGATTCAGTCAATATGTCCTTGTCCTTATCGAAGGACTCTGGCACAATAATCG | 1740 |
| Dp | 1681 | GAGGAGTTCATGATTCAGTCAATATGTCCTTGTCCTTATCGAAGGACTCTGGCACAATAATCG | 1740 |
| Qy | 1741 | TATTCATTAAACCGGAGGTAGATGAGATGAGCAACGCTGTACATGACTGAAATCC | 1800 |
| Dp | 1741 | TATTCATTAAACCGGAGGTAGATGAGATGAGCAACGCTGTACATGACTGAAATCC | 1800 |
| Qy | 1801 | TGCTATATCCGTTTATGAAATCCATGATATATATTTTGTGATGATTTGGAGCTTTTGTTC | 1860 |
| Dp | 1801 | TGCTATATCCGTTTATGAAATCCATGATATATATTTTGTGATGATTTGGAGCTTTTGTTC | 1860 |
| Qy | 1861 | ACGTTCAAAATTTTTTGTGCAACCCCTTTTGTGAAACGAAACAACGCGTATGGCTGCGAATG | 1920 |
| Dp | 1861 | ACGTTCAAAATTTTTTGTGCAACCCCTTTTGTGAAACGAAACAACGCGTATGGCTGCGAATG | 1920 |
| Qy | 1921 | CCCATACTGTTGAGCAATTCAGTTCAATTATAAATGTCGTCGCGGCGCAACTGCAACT | 1980 |
| Dp | 1921 | CCCATACTGTTGAGCAATTCAGTTCAATTATAAATGTCGTCGCGGCGCAACTGCAACT | 1980 |
| Qy | 1981 | CCGATTAATAACGCGGCCCAACAACCGGCTAAAGAAATGGAAGAAGTTTCACTGCAATCG | 2040 |
| Dp | 1981 | CCGATTAATAACGCGGCCCAACAACCGGCTAAAGAAATGGAAGAAGTTTCACTGCAATCG | 2040 |
| Qy | 2041 | ACGATTTCTGATTTTGTATTCAGCCCAATGCTTTCATAGCTTCTGCAACCGAACCGGAC | 2100 |
| Dp | 2041 | ACGATTTCTGATTTTGTATTCAGCCCAATGCTTTCATAGCTTCTGCAACCGAACCGGAC | 2100 |
| Qy | 2101 | ATTTCGAAGTACTCAGCGTAAGTATGTCACCTCGATATGTCATCTGTAAGCAATT | 2160 |
| Dp | 2101 | ATTTCGAAGTACTCAGCGTAAGTATGTCACCTCGATATGTCATCTGTAAGCAATT | 2160 |
| Qy | 2161 | GTTCCAGGAACCAAGGCGTATCTCTTCAATACCTTAATGCAATGCTCTCCAGCGTTTCCA | 2220 |
| Dp | 2161 | GTTCCAGGAACCAAGGCGTATCTCTTCAATACCTTAATGCAATGCTCTCCAGCGTTTCCA | 2220 |
| Qy | 2221 | TCTTCACAGGATTAAGATGCGCGCGGCGCTTCTTTATGATTTTGTGCGCTCTTCATGSGGA | 2280 |
| Dp | 2221 | TCTTCACAGGATTAAGATGCGCGCGGCGCTTCTTTATGATTTTGTGCGCTCTTCATGSGGA | 2280 |
| Qy | 2281 | CGTCGGTGTGTTACGTTTGATTTTCTTGAAGTTTAAAGATTCTGTCTCATGATGAC | 2340 |
| Dp | 2281 | CGTCGGTGTGTTACGTTTGATTTTCTTGAAGTTTAAAGATTCTGTCTCATGATGAC | 2340 |
| Qy | 2341 | GCTCTACGAGACCTCCCGGGCACTCTCGACACCCCTATGCGGAGTAAACCAAAAGGCTTT | 2400 |
| Dp | 2341 | GCTCTACGAGACCTCCCGGGCACTCTCGACACCCCTATGCGGAGTAAACCAAAAGGCTTT | 2400 |
| Qy | 2401 | TCGCGAACCAACATACCTCGGCTATGCAAGTCTTGTGCGGGGCGACGCGCCAAATCTCCAGGCAT | 2460 |
| Dp | 2401 | TCGCGAACCAACATACCTCGGCTATGCAAGTCTTGTGCGGGGCGACGCGCCAAATCTCCAGGCAT | 2460 |
| Qy | 2461 | TGAGCGGGGTTATCCAAAGAAAGAACCGCGTGTCTCTGCAATTCGCGTGTATCTACCGGT | 2520 |
| Dp | 2461 | TGAGCGGGGTTATCCAAAGAAAGAACCGCGTGTCTCTGCAATTCGCGGTTACTACCGGT | 2520 |
| Qy | 2521 | TCCGAGACCACTATGCGTCTTCCCGGAGAGGGGGGGTCTTGAGGCTGACGACACTCATTA | 2580 |
| Dp | 2521 | TCCGAGACCACTATGCGTCTTCCCGGAGAGGGGGGGTCTTGAGGCTGACGACACTCATTA | 2580 |

QY 2581 CTAAGCCATGAGCTGAGAGCTTTTCGCGTGAAGACAGTAGTTCTCACAGGGGAGTAGTT 2640
DB 2581 CTAAGCCATGAGCTGAGAGCTTTTCGCGTGAAGACAGTAGTTCTCACAGGGGAGTAGTT 2640
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DB 2701 TGGCGCGCGCTGGGCAACATTCCAGGGGACCTGTCCTCGGTAAATGGCGAATGGGACCC 2760
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RESULT 2
US-10-066-130-17
Sequence 17, Application US/10066130
Patent No. 6699657
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
TITLE OF INVENTION: Viruses
FILE REFERENCE: PH-7171 NP
CURRENT APPLICATION NUMBER: US/10/066,130
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/265,437
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 5860
TYPE: DNA
ORGANISM: Viral
US-10-066-130-17

Query Match 100.0%; Score 2771; DB 4; Length 5860;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 CCAGAGTATGAGAGGCTTTTATGAGGCTTAGGCTTTTGAAGAAAGCTTACATGATC 360
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DB 1741 TATTCATTTAAAAACGGAGAGGTAGATGATGATGACGAACTGTATCATGCACTAAATCCC 1800
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DB 1801 TGGTAAATCCGTTTAAATCATGATPAATAATTTTGGATGATGAGAGCTTTTGGC 1860
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DB 1861 AGCTTCAAAATTTTGGCAACCCCTTTTGGAAACGAAACACAGGATGCGAAATG 1920
QY 1921 CCCATACGTTGAGCAATTCACGTTCAATTAATGTCGTCGCGGCGCACTGCAACT 1980
DB 1921 CCCATACGTTGAGCAATTCACGTTCAATTAATGTCGTCGCGGCGCACTGCAACT 1980
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DB 1981 CCGATTAATAACCGGCCCAACCGGCAATAAGAAATTTGAGATGAGAGCTTTCATGCAATG 2040
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DB 2041 AGCATTCGTGATTTGATTCAGCCCATATGCTTTCACTCTGCGCAACGGAACGAG 2100
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DB 2341 GGTTCAGAGAGCTCCCGGCGCACTGCAAGCACTTATAGGACGATGACCAAGGCTT 2400
QY 2401 TCGGACCCCAACCTACTCGGCTAGCAGTCTTGCGGGGCAACGCCAATCTCAAGCAT 2460
DB 2401 TCGGACCCCAACCTACTCGGCTAGCAGTCTTGCGGGGCAACGCCAATCTCAAGCAT 2460
QY 2461 TGAAGCGGGTTATTCAGAAAGAACCGGTCGTCTTGCAATTCGCGTGTACTCACCGGT 2520
DB 2461 TGAAGCGGGTTATTCAGAAAGAACCGGTCGTCTTGCAATTCGCGTGTACTCACCGGT 2520
QY 2521 TCGGACAGCACTATGCGCTCTCCCGGAGGGGGGCTCTGAGGCTGCAAGCACTCATTA 2580
DB 2521 TCGGACAGCACTATGCGCTCTCCCGGAGGGGGGCTCTGAGGCTGCAAGCACTCATTA 2580
QY 2581 CTAAGCGCAATGCTAGCGCTTCTGCTGTAAGAAGTATCTCTCAAGGGAGTGATTT 2640
DB 2581 CTAAGCGCAATGCTAGCGCTTCTGCTGTAAGAAGTATCTCTCAAGGGAGTGATTT 2640

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QY 2701 TGGCGCGGCTGGGCAACATTTCCGAGGGGACCGTCCCTCTCGGTAATGGGAATGGACCC 2760
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DB 2761 ACAATCTCTC 2771

RESULT 3
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; Sequence 19, Application US/10066130
; Patent No. 6639657
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase (I
; FILE REFERENCE: PH-7171 NP
; CURRENT APPLICATION NUMBER: US/10/066,130
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/265,437
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: viral
US-10-066-130-19

Query Match 96.5%; Score 2674; DB 4; Length 2674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAATCCGCTGTGGAATGATGTGTCAGTTAGGGTGTGAAAGTCCCGAGCTCCCGACAG 60
DB 1 GGAATCCGCTGTGGAATGATGTGTCAGTTAGGGTGTGAAAGTCCCGAGCTCCCGACAG 60
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QY 181 GCCCTTAATCCGCCCATCCGCCCTTAATCTCGGCCAATTCGCGCCCA 240
DB 181 GCCCTTAATCCGCCCATCCGCCCTTAATCTCGGCCAATTCGCGCCCA 240
QY 241 TGGCTGACTAATTTTTTTTATTTATGACAGAGCCGAGCGGCTCGGCTGTAGCTAAT 300
DB 241 TGGCTGACTAATTTTTTTTATTTATGACAGAGCCGAGCGGCTCGGCTGTAGCTAAT 300
QY 301 CCAAGATGATGAGAGGCTTTTTTGGAGGCTTGGAGCTTTTGCAAAAGCTTAACATGATC 360
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QY 361 TGCAGAGAGCCAGTATCAGCACTCTCTGACGATGCGGCTCAAGGACCTTTCAAGCT 420
DB 361 TGCAGAGAGCCAGTATCAGCACTCTCTGACGATGCGGCTCAAGGACCTTTCAAGCT 420
QY 421 AGCGGTGACTAGGCTTAAATGAGGCAACATTTAAAGAAAGAAAGAAAGAAAGAA 480
DB 421 AGCGGTGACTAGGCTTAAATGAGGCAACATTTAAAGAAAGAAAGAAAGAAAGAA 480
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RESULT 4
US-10-066-130-20
; Sequence 20. Application US/10066130
; Patent No. 6693657
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171 NP
; CURRENT APPLICATION NUMBER: US/10/066,130
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/265,437
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 2327
; TYPE: DNA
; ORGANISM: viral
US-10-066-130-20

Query Match 84.0%; Score 2327; DB 4; Length 2327;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 348 AGCTTACATGATCTGCAGAGAGCGCATATCAGACACTCTGCGAGTCATGCGGCTCAGG 407
Db 1 AGCTTACATGATCTGCAGAGAGCGCATATCAGACACTCTGCGAGTCATGCGGCTCAGG 60
QY 408 ACCTTTCAAGCTAGCCGTGCTAGAGGCTAAGATGAGCCACATTTAAAGAAAGAA 467
Db 61 ACCTTTCAAGCTAGCCGTGCTAGAGGCTAAGATGAGCCACATTTAAAGAAAGAA 120
QY 468 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 527
Db 121 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 180
QY 528 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 587
Db 181 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240
QY 588 AAATGCGCTTAAGAGCGCGGAGTGTTAACCCCAACCTTTAAACGCGCATCTTTCGCGCTT 647
Db 241 AAATGCGCTTAAGAGCGCGGAGTGTTAACCCCAACCTTTAAACGCGCATCTTTCGCGCTT 300
QY 648 CTTGGCTTTATGAGATCTCTGATTTTCTTGGCTGAGATTTCGCGTAAGACCTTT 707
Db 301 CTTGGCTTTATGAGATCTCTGATTTTCTTGGCTGAGATTTCGCGTAAGACCTTT 360
QY 708 CGGTAAGCTGATGCAAAACAACCTCTCGCGGCACTTTTGGCGGTGTTACTTGACT 767
Db 361 CGGTAAGCTGATGCAAAACAACCTCTCGCGGCACTTTTGGCGGTGTTACTTGACT 420
QY 768 GAGGAGCTAATCCAGATCTCTTTTCCGTCATCGTCTTTCGCTGCTCAAAAACAAC 827
Db 421 GAGGAGCTAATCCAGATCTCTTTTCCGTCATCGTCTTTCGCTGCTCAAAAACAAC 480
QY 828 GGGCGGCGGAAAGTTCACCGCGCTCATGTCGGAAGACCTGCGACACCTGCGTGAAGAT 887
Db 481 GGGCGGCGGAAAGTTCACCGCGCTCATGTCGGAAGACCTGCGACACCTGCGTGAAGAT 540
QY 888 GTTGGGGTGTGGAGCAAGATGGATTCCAATTCAGCGGGAAGCAACCTGATAGGCTTTGTA 947
Db 541 GTTGGGGTGTGGAGCAAGATGGATTCCAATTCAGCGGGAAGCAACCTGATAGGCTTTGTA 600
QY 948 CTTAATCAGAGACTTTCAGCGGCTCAACGATGAAGATGTTGCTGCTTCCAGTAAGC 1007
Db 601 CTTAATCAGAGACTTTCAGCGGCTCAACGATGAAGATGTTGCTGCTTCCAGTAAGC 660
QY 1008 TATGCTCCAGATGATGCAATCCATCTTGTCAATCAAGCGGTGCTTCCGATTT 1067
Db 661 TATGCTCCAGATGATGCAATCCATCTTGTCAATCAAGCGGTGCTTCCGATTT 720
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QY 1068 GTTTACATAACCGGACATATCATATGAGACCTCTCAACAAGTTCCGCTTTGATTAAC 1127
Db 721 GTTTACATAACCGGACATATCATATGAGACCTCTCAACAAGTTCCGCTTTGATTAAC 780
QY 1128 GCCACGCTTTTCCGGATTCAGATCCAAACCTTCGCTTCAAAAATGAAACAACCTT 1187
Db 781 GCCACGCTTTTCCGGATTCAGATCCAAACCTTCGCTTCAAAAATGAAACAACCTT 840
QY 1188 ACCGACCGGCGCGGTTTATCCATCCCGCTCGGCTGTAATCAGAAATGCGATGATC 1247
Db 841 ACCGACCGGCGCGGTTTATCCATCCCGCTCGGCTGTAATCAGAAATGCGATGATC 900
QY 1248 AGTAGCCCATATCTTGGCTGATATCTGAGATGGAACCTTCTGGCAACCGCTTCCG 1307
Db 901 AGTAGCCCATATCTTGGCTGATATCTGAGATGGAACCTTCTGGCAACCGCTTCCG 960
QY 1308 GACTTCTTTAGAGAGGGAGCGCCACAGAGCAATTTGCTGTAATTAATGATTAATGCTTA 1367
Db 961 GACTTCTTTAGAGAGGGAGCGCCACAGAGCAATTTGCTGTAATTAATGATTAATGCTTA 1020
QY 1368 TTTGTCAATCAGATGCTTTTGGCGAAGAGAAATAGGGTTGGACCAAGCGGCACT 1427
Db 1021 TTTGTCAATCAGATGCTTTTGGCGAAGAGAAATAGGGTTGGACCAAGCGGCACT 1080
QY 1428 TTGAATCTTGTAAATCTGAAGGCTCTCAAGAAACAGCTCTTCTTCAATCTATACATTA 1487
Db 1081 TTGAATCTTGTAAATCTGAAGGCTCTCAAGAAACAGCTCTTCTTCAATCTATACATTA 1140
QY 1488 GAGACTCGAATTCACATATCAATATATCGAGTGTATGAACATTCGAAACCGTGATG 1547
Db 1141 GAGACTCGAATTCACATATCAATATATCGAGTGTATGAACATTCGAAACCGTGATG 1200
QY 1548 GAATGGAACAACAACCTTAATATGCAATATCCGGAATGATTAATGTCGCAAAAATAGATG 1607
Db 1201 GAATGGAACAACAACCTTAATATGCAATATCCGGAATGATTAATGTCGCAAAAATAGATG 1260
QY 1608 TCTGCGATCGAAGATCTCAACGAGGAGTCTATGAGCGAGACAGACCTTTAGGCA 1667
Db 1261 TCTGCGATCGAAGATCTCAACGAGGAGTCTATGAGCGAGACAGACCTTTAGGCA 1320
QY 1668 ACCAGTATCCAGAGAGTCAATGATCAATGCAATGCTTCTGTCCTATCCGAAAGACTC 1727
Db 1321 ACCAGTATCCAGAGAGTCAATGATCAATGCAATGCTTCTGTCCTATCCGAAAGACTC 1380
QY 1728 TGGCAAAAATGATATCTTAATAACCGGAGATGATGATGATGACGAACGTGATC 1787
Db 1381 TGGCAAAAATGATATCTTAATAACCGGAGATGATGATGATGACGAACGTGATC 1440
QY 1788 CGAGTAATCCCTGATATCCGTTTAAATTCATGATTAATTAATTTTGGATGATG 1847
Db 1441 CGAGTAATCCCTGATATCCGTTTAAATTCATGATTAATTAATTTTGGATGATG 1500
QY 1848 GAGCTTTTGTGACGCTCAAAATTTTGGAAACCCCTTTTGGAAACGAACACACGCT 1907
Db 1501 GAGCTTTTGTGACGCTCAAAATTTTGGAAACCCCTTTTGGAAACGAACACACGCT 1560
QY 1908 AGGCTCGGAATGCGCATCTGTTGAGCAATTCAGCTTATTAATATGTCGTCGCGG 1967
Db 1561 AGGCTCGGAATGCGCATCTGTTGAGCAATTCAGCTTATTAATATGTCGTCGCGG 1620
QY 1968 CGCAATCGCACTCGATTAATTAACGCGCCAAACCGGCAATTAAGAAATGGAAGAGTT 2027
Db 1621 CGCAATCGCACTCGATTAATTAACGCGCCAAACCGGCAATTAAGAAATGGAAGAGTT 1680
QY 2028 TTCACTGATACAGAGATCTGATATTTGATTCAGCCCATATCGTTTATAGCTTCTG 2087
Db 1681 TTCACTGATACAGAGATCTGATATTTGATTCAGCCCATATCGTTTATAGCTTCTG 1740
QY 2088 CAACGGAAGGACATTTGGAATGCTCAGCGTAAAGTGTCACTCGATATGTCATC 2147
Db 1741 CAACGGAAGGACATTTGGAATGCTCAGCGTAAAGTGTCACTCGATATGTCATC 1800
QY 2148 TGTAAAGCAATTTGTTCCAGAAACGAGGCGTATCTTCAATAGCCTTATGAGTTGCTC 2207
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Db 1801 TGTAAAGCAATGTTTCAGAGAACAGGGGATCTCTTCATAGCCTTATGCACTGCTC 1860
QY 2208 TCCAGGAGTTTCCATCTTCCAGCGGATAGAAATGGCGCGGGCCTTTCTTATATGTTTTGGC 2267
Db 1861 TCCAGGAGTTTCCATCTTCCAGCGGATAGAAATGGCGCGGGCCTTTCTTATATGTTTTGGC 1920
QY 2268 GTCTTCATAGGAGAGTGTGGTTGTATAGTTTGTGTTTCTTGTAGAGTTTATGATTCGT 2327
Db 1921 GTCTTCATAGGAGAGTGTGGTTGTATAGTTTGTGTTTCTTGTAGAGTTTATGATTCGT 1980
QY 2328 GCTCATGATGACGAGTCTTACGAGACCTCCGCGGAGCATCTGCAAGCACTTATGAGCACT 2387
Db 1981 GCTCATGATGACGAGTCTTACGAGACCTCCGCGGAGCATCTGCAAGCACTTATGAGCACT 2040
QY 2388 ACCACAGGAGCTTTCCGCGACCCCAACATCTAGTGGCTTATGAGAGTCTTGGGGGAGCAAGCCCA 2447
Db 2041 ACCACAGGAGCTTTCCGCGACCCCAACATCTAGTGGCTTATGAGAGTCTTGGGGGAGCAAGCCCA 2100
QY 2448 AATCTCCAGGAGTGTGAGCGGGGTTTATCCAGAAAGAACCGGAGTCTCTGCAATTCGGG 2507
Db 2101 AATCTCCAGGAGTGTGAGCGGGGTTTATCCAGAAAGAACCGGAGTCTCTGCAATTCGGG 2160
QY 2508 TGTACTCACCGGTTCCGCAAGACCACTATGCTCTCCCGGAGGGGGGATCTTGGAGGCTG 2567
Db 2161 TGTACTCACCGGTTCCGCAAGACCACTATGCTCTCCCGGAGGGGGGATCTTGGAGGCTG 2220
QY 2568 CACGACACTCATCTAACCAGCATAGCTTCTGCTGCTTATGAGAGTCTTCTCA 2627
Db 2221 CACGACACTCATCTAACCAGCATAGCTTCTGCTGCTTATGAGAGTCTTCTCA 2280
QY 2628 CAGGGAGAGTTCATGAGTGTGAGTGTGCGCCCATAGAGGGGGGCTGGC 2674
Db 2281 CAGGGAGAGTTCATGAGTGTGAGTGTGCGCCCATAGAGGGGGGCTGGC 2327

RESULT 5
US-09-743-194-28/C
Sequence 28, Application US/09743194
Patent No. 6718601
GENERAL INFORMATION:
APPLICANT: Belfield, Graham
APPLICANT: Oakley, Caroline
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
Controlling Nucleic Acid Expression in Yeast
FILE REFERENCE: 3526.82543
CURRENT APPLICATION NUMBER: US/09/743,194
CURRENT FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 13654
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
US-09-743-194-28

Query Match 59.8%; Score 1656.4; DB 4; Length 13654;
Best Local Similarity 98.8%; Pred. No. 2.5e-303;
Matches 1669; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 624 TTAAGAGGAGATTTTCCGCCCTTCTTGCCCTTATAGAGATCTCTGATTTTTTCTTGC 683
Db 2868 TTAAGAGGAGATTTTCCGCCCTTCTTGCCCTTATAGAGATCTCTGATTTTTTCTTGC 2809
QY 684 GTTCGATTTTCCGTTAAGACCTTTCCGTTACTTGTCCACAACAACAACACTCTCCGCGCAA 743
Db 2808 GTTCGATTTTCCGTTAAGACCTTTCCGTTACTTGTCCACAACAACAACACTCTCCGCGCAA 2749
QY 744 CTTTTCGCGGTTTGTACTTGTAGTGGAGAGTAATCCAGATCTTTTTCGCTCATCGT 803
Db 2748 CTTTTCGCGGTTTGTACTTGTAGTGGAGAGTAATCCAGATCTTTTTCGCTCATCGT 2689
QY 804 CTTTTCGCTGTCCAAAACAACAAGCGGGGGAAGTTTCAACGCGCTCATCTGCGGGAAG 863

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Db 2688 CTTTCGCTGTCCAAAACAACAAGCGGGGGAAGTTTCAACGCGCTCATCTGCGGGAAG 2629
QY 864 ACTCGGACACCTGGGTGGAAGATGTGGGGGTTGAGAGCAAGATGATTCATTCAC 923
Db 2628 ACTCGGACACCTGGGTGGAAGATGTGGGGGTTGAGAGCAAGATGATTCATTCAC 2569
QY 924 GGAAGCACTGATAGCTTTGATTAATCAGACCTTCAGCGGTCAACATGAAGA 983
Db 2568 GGAAGCACTGATAGCTTTGATTAATCAGACCTTCAGCGGTCAACATGAAGA 2509
QY 984 GTTTCGTTCTGTCCAGTAAGCTATGTCTCAGAAATGTAACATTCATCTTGTCAAT 1043
Db 2508 GTTTCGTTCTGTCCAGTAAGCTATGTCTCAGAAATGTAACATTCATCTTGTCAAT 2449
QY 1044 CAAAGCGTTGTGCTTCCGGAATGTTTATCAATACCGGACATTAATCATAGACCTTCAC 1103
Db 2448 CAAAGCGTTGTGCTTCCGGAATGTTTATCAATACCGGACATTAATCATAGACCTTCAC 2389
QY 1104 ACACAGTTGAGCTTTGATTAAGCGCCAGGCTTTCCGGTATCCAGATCCAACTT 1163
Db 2388 ACACAGTTGAGCTTTGATTAAGCGCCAGGCTTTCCGGTATCCAGATCCAACTT 2329
QY 1164 CGCTTCAAAAATGGAACAACCTTACCGACCGCGCCGTTTATCATCCCTCGGGTGT 1223
Db 2328 CGCTTCAAAAATGGAACAACCTTACCGACCGCGCCGTTTATCATCCCTCGGGTGT 2269
QY 1224 AATCAGATAGCTATGATGATGTCATGAGGCCATATCTTCCGTATCTCGGAGATG 1283
Db 2268 AATCAGATAGCTATGATGATGTCATGAGGCCATATCTTCCGTATCTCGGAGATG 2209
QY 1284 GAACCTCTTGGCAACCGCTTCCCGACCTTCTTACAGAGGGAGGCGCACGAAGCAT 1343
Db 2208 GAACCTCTTGGCAACCGCTTCCCGACCTTCTTACAGAGGGAGGCGCACGAAGCAT 2149
QY 1344 TTCGTAAATTAATGATTAATCGTATTTGTCAATCAGAGTCTTTTGGCAAGAGAGA 1403
Db 2148 TTCGTAAATTAATGATTAATCGTATTTGTCAATCAGAGTCTTTTGGCAAGAGAGA 2089
QY 1404 TTAGGTTGGCACACGAGCGCATTTGAATCTTGTATCTTGAAGCTCTCAGAAACAG 1463
Db 2088 TTAGGTTGGCACACGAGCGCATTTGAATCTTGTATCTTGAAGCTCTCAGAAACAG 2029
QY 1464 CTCCTTTCATATCTATATCAATTAAGACCTGGAATCCATATCAATATCCAGTGT 1523
Db 2028 CTCCTTTCATATCTATATCAATTAAGACCTGGAATCCATATCAATATCCAGTGT 1969
QY 1524 AGTAAACATTCGAAAACCGTATGGAATGGAACAACACTTAATTCGAGTATCCGGAAT 1583
Db 1968 AGTAAACATTCGAAAACCGTATGGAATGGAACAACACTTAATTCGAGTATCCGGAAT 1909
QY 1584 GATTTGATTCGAAAATATGAGTCTCTGCGATCGAGAAATCTCAGCGAGCGATCTATG 1643
Db 1908 GATTTGATTCGAAAATATGAGTCTCTGCGATCGAGAAATCTCAGCGAGCGATCTATG 1849
QY 1644 AGCGAGAGGACACCTTTAAGGAGACAGTATATCCAGGGATCATGATATAGGCAAT 1703
Db 1848 AGCGAGAGGACACCTTTAAGGAGACAGTATATCCAGGGATCATGATATAGGCAAT 1789
QY 1704 TGTCTTGTCCATGGAAGGACTCTGGGACAAAATCGTATTCATTAACCGGGAGGTAG 1763
Db 1788 TGTCTTGTCCATGGAAGGACTCTGGGACAAAATCGTATTCATTAACCGGGAGGTAG 1729
QY 1764 ATGAGATGAGCAAGAGTGTATCATGCACTGAATCCCTGTATATCCGTTTGAATTCAT 1823
Db 1728 ATGAGATGAGCAAGAGTGTATCATGCACTGAATCCCTGTATATCCGTTTGAATTCAT 1669
QY 1824 GATTAATATTTTGGATGATGAGAGCTTTTGTGACGTTCAAAATTTTGGCAACC 1883
Db 1668 GATTAATATTTTGGATGATGAGAGCTTTTGTGACGTTCAAAATTTTGGCAACC 1609
QY 1884 CTTTTCGAAAAGAACACGAGTGAAGCTGCAAAATGCCATATCTTGAGCAATTCACG 1943

Dh 1608 CTTTGGAAACGAACACACGATAGGCTGGAAATGCCATACGTGTGAGCAATTCACG 1549
Qy 1344 TTCTATTAAATGTCGTCGCGGCGCACTGCACTCCGATAATAACCGCGCCCAAC 2003
Dh 1548 TTCTATTAAATGTCGTCGCGGCGCACTGCACTCCGATAATAACCGCGCCCAAC 1489
Qy 2004 CGGATTAAGAAATGAGAGAGTTTTCATCATGACGACATTCGTGATTTGATTCAG 2063
Dh 1488 CGGATTAAGAAATGAGAGAGTTTTCATCATGACGACATTCGTGATTTGATTCAG 1429
Qy 2064 CCATATCGTTTCATAGCTTTCGCCAACGAAACGACATTTGAACTACAGCTTAAGT 2123
Dh 1428 CCATATCGTTTCATAGCTTTCGCCAACGAAACGACATTTGAACTACAGCTTAAGT 1369
Qy 2124 GATGTCCACCTCGATATGTCATCTGTAAAGCAATTTGTCAGAAACGAGGCGTATCT 2183
Dh 1368 GATGTCCACCTCGATATGTCATCTGTAAAGCAATTTGTCAGAAACGAGGCGTATCT 1309
Qy 2184 CTTGATAGCCTTATGACGTTGCTCTCCAGCGGTTCCATCTTCCAGCGGATAGAAATGCGC 2243
Dh 1308 CTTGATAGCCTTATGACGTTGCTCTCCAGCGGTTCCATCTTCCAGCGGATAGAAATGCGC 1249
Qy 2244 CGGACCTTTCTTTATGTTTTGGCGTCTCCATGGAAGTCGATGGTGTACGTTTGT 2303
Dh 1248 CGGACCTTTCTTTATGTTTTGGCGTCTCCATGGAAGTCGATGGTGTATAGCT 1189
Qy 2304 TTTTCTTTGA 2313
Dh 1188 TGTTTTTTTA 1179

RESULT 6

US-09-602-628-7/c
; Sequence 7, Application US/09602628
; Patent No. 649535
; GENERAL INFORMATION:
; APPLICANT: Eames, Brian
; APPLICANT: Contag, Christopher
; TITLE OF INVENTION: Red-Shifted Luciferase
; FILE REFERENCE: SUN-127
; CURRENT APPLICATION NUMBER: US/09/602,628
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/140,598
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: pGL3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1650)
US-09-602-628-7

Query Match 59.7%; Score 1655.6; DB 4; Length 1686;
Best Local Similarity 98.9%; Pred. No. 2.3e-303;
Matches 1667; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 591 TGGGCTTAAGAGGCGGAGTGTTCACCCCACTTTAAAGCGAGATCTTTCCGCGCTTCT 650
Dh 1686 TGTCTGAAGGCGGCGCGCCGCGACTCTGAATTAACAGGCAATCTTTCCGCGCTTCT 1627
Qy 651 GGCCTTTATGAGATCTCTGTATTTTCTGCGTCGAGTTTCCGTAAGACCTTTCCG 710
Dh 1626 GGCCTTTATGAGATCTCTGTATTTTCTGCGTCGAGTTTCCGTAAGACCTTTCCG 1567
Qy 711 TACTTCTCAACAAACAACTCTCCGCGCACTTTTCCGCGTGTATCTTGAATGCGC 770
Dh 1566 TACTTCTCAACAAACAACTCTCCGCGCACTTTTCCGCGTGTATCTTGAATGCGC 1507
Qy 771 GAGTAATCAGATCTCTTTTCCGTCATGTCCTTCCGAGCTCCAAACAAACAGCGC 830
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Dh 1506 GAGTAATCAGATCTCTTTTCCGTCATGTCCTTCCGTCCTCCAAACAAACAGCGC 1447
Qy 831 GCGGGAAGTTTCAACCGCGCTCATGTCGGAGAACCTGCGACACTCGCGTGAAGATTT 890
Dh 1446 GCGGGAAGTTTCAACCGCGCTCATGTCGGAGAACCTGCGACACTCGCGTGAAGATTT 1387
Qy 891 GGGGTGTGAGCAAGATGGAATTCGAATTCAGGGGAGCCACTGATAGCTTTGATCTT 950
Dh 1386 GGGGTGTGAGCAAGATGGAATTCGAATTCAGGGGAGCCACTGATAGCTTTGATCTT 1327
Qy 951 AATCAGAGACTTCAAGCGCGTCAACGATGGAAGATGTCGTCCTTCCAGTAAGCTAT 1010
Dh 1326 AATCAGAGACTTCAAGCGCGTCAACGATGGAAGATGTCGTCCTTCCAGTAAGCTAT 1267
Qy 1011 GTCTCCGAATGTAGCCATTCATCTTGTCAATCAAGCGTGTGCGCTTCCGATTTGT 1070
Dh 1266 GTCTCCGAATGTAGCCATTCATCTTGTCAATCAAGCGTGTGCGCTTCCGATTTGT 1207
Qy 1071 TACATAACGGAGATATATCATAGGACCTTCACACAGTTGCGCTTGTATTAAGCGC 1130
Dh 1206 TACATAACGGAGATATATCATAGGACCTTCACACAGTTGCGCTTGTATTAAGCGC 1147
Qy 1131 CAGCGTTTCCGCGTATCCAGATTCACAACTTCGCTTCAAAAATGGAACAACTTACC 1190
Dh 1146 CAGCGTTTCCGCGTATCCAGATTCACAACTTCGCTTCAAAAATGGAACAACTTACC 1087
Qy 1191 GACCGCGCGCGGTTATCATCCCTCGGCGTGAATCAAGATGCTGATGTCATG 1250
Dh 1086 GACCGCGCGCGGTTATCATCCCTCGGCGTGAATCAAGATGCTGATGTCATG 1027
Qy 1251 GAGCCCATATCCCTGCTGATATCTTGGCAGATGGAACCTTGGGCAACCGCTTCCCGAC 1310
Dh 1026 GAGCCCATATCCCTGCTGATATCTTGGCAGATGGAACCTTGGGCAACCGCTTCCCGAC 967
Qy 1311 TTCTTGAAGAGGAGCGCCACAGAAACAAATTTGCTGAATTAATGATTAATCGATTT 1370
Dh 966 TTCTTGAAGAGGAGCGCCACAGAAACAAATTTGCTGAATTAATGATTAATCGATTT 907
Qy 1371 GTCAATCAAGTCTTTTGGCGAAGAGAAATAGGTTGGCACGACGCGACCTTTG 1430
Dh 906 GTCAATCAAGTCTTTTGGCGAAGAGAAATAGGTTGGCACGACGCGACCTTTG 847
Qy 1431 AATCTTGAATCCTGAAGGCTCCTCGAAGAACGCTCTTTCGAAATCTATACCTTAAGC 1490
Dh 846 AATCTTGAATCCTGAAGGCTCCTCGAAGAACGCTCTTTCGAAATCTATACCTTAAGC 787
Qy 1491 GACTCGAAATCCACATATCAAAATATCCGAGTGAATTAACATTCGAAACCGGATGGA 1550
Dh 786 GACTCGAAATCCACATATCAAAATATCCGAGTGAATTAACATTCGAAACCGGATGGA 727
Qy 1551 TGGAAACAACCTTAATAATCGCAGTATCCGAAATGATTTGATTCGAAATAAGATCTCT 1610
Dh 726 TGGAAACAACCTTAATAATCGCAGTATCCGAAATGATTTGATTCGAAATAAGATCTCT 667
Qy 1611 GGCATCGAGAAATCTACGCAAGCACTTCTATGAGGCAAGGCAACCTTTAGGCGAGC 1670
Dh 666 GGCATCGAGAAATCTACGCAAGCACTTCTATGAGGCAAGGCAACCTTTAGGCGAGC 607
Qy 1671 AGTAGATCCAGAGAGATTCATGATCAGTCAATTTGCTTCCCTATCGAAGGACTCTGG 1730
Dh 606 AGTAGATCCAGAGAGATTCATGATCAGTCAATTTGCTTCCCTATCGAAGGACTCTGG 547
Qy 1731 CACAAATCGTATCTTAAACCGGAGGTAGATGAGATGTCAGCAAGTGTATCTGA 1790
Dh 546 CACAAATCGTATCTTAAACCGGAGGTAGATGAGATGTCAGCAAGTGTATCTGA 487
Qy 1791 CTGAATTCCTGTAATCCGTTTGAATTCATGATTAATTTTGTGATGATTTGGAG 1850
Dh 486 CTGAATTCCTGTAATCCGTTTGAATTCATGATTAATTTTGTGATGATTTGGAG 427
Qy 1851 CTTTTCCTCAGGTTCAAAATTTTTCGAAACCGCTTTTGAAGAGCAACCAAGGATAG 1910
Dh 426 CTTTTCCTCAGGTTCAAAATTTTTCGAAACCGCTTTTGAAGAGCAACCAAGGATAG 367

QY 2004 CGGATTAAGATTAAGAGAGTTTTCATGCTGATACGACGATTCGTGATTTGTATTG 2063
Db 788 CGGATTAAGATTAAGAGAGTTTTCATGCTGATACGACGATTCGTGATTTGTATTG 729
QY 2064 CCCATATGCTTTCATAGCTTCTGCGCAACCGAAGCGACATTTGCAAGTACTGAGGTAAGT 2123
Db 728 CCCATATGCTTTCATAGCTTCTGCGCAACCGAAGCGACATTTGCAAGTACTGAGGTAAGT 669
QY 2124 GATGTCACCTCGATATGTCATCTGTAAAGCAATTGTTCCAGGAAACGAGGCGTATCT 2183
Db 668 GATGTCACCTCGATATGTCATCTGTAAAGCAATTGTTCCAGGAAACGAGGCGTATCT 609
QY 2184 CTTGATAGCCTTATGAGCTGCTCCAGCGGTTCCATCTTCCAGCGGATATGAGCCG 2243
Db 608 CTTGATAGCCTTATGAGCTGCTCCAGCGGTTCCATCTTCCAGCGGATATGAGCCG 549
QY 2244 CGGACCTTCTTATGTTTGGCGTCTTCATGAGGACGTGCGTTGGTGTACCTTTGGT 2303
Db 548 CGGACCTTCTTATGTTTGGCGTCTTCATGATATGATATATAACGTATTTTGT 489
QY 2304 TTTTCTTTGAGCTTT 2318
Db 488 ATGTTCTTTGATTT 474

RESULT 8
US-09-577-424-3/c
; Sequence 3, Application US/09577424
; Patent No. 6525245
; GENERAL INFORMATION:
; APPLICANT: Rhoads, David M
; TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
; FILE REFERENCE: UNL2990
; CURRENT APPLICATION NUMBER: US/09/577,424
; NUMBER OF SEQ. ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ. ID NO. 3
; LENGTH: 14194
; TYPE: DNA
; ORGANISM: Bacterial Plasmid DNA-Plasmid pZB-ALN
US-09-577-424-3

Query Match 59.7%; Score 1654.2; DB 4; Length 14194;
Best Local Similarity 99.8%; Pred. No. 6,7e-303;
Matches 1656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 624 TTAAACGGCGATCTTCCGCCCTTCTGCGCTTATGAGATCTCTGATTTTCTTGC 683
Db 13826 TTAAACGGCGATCTTCCGCCCTTCTGCGCTTATGAGATCTCTGATTTTCTTGC 13767
QY 684 GTCGAGTTTTCGGGTAGACCTTTCGGTACTTCGTCACAAACACACTCTCCGCGCAA 743
Db 13766 GTCGAGTTTTCGGGTAGACCTTTCGGTACTTCGTCACAAACACACTCTCCGCGCAA 13707
QY 744 CTTTTCGCGGTTGTTACTGACTGCGACGTAAATCCAGATCTTTTTCGCGTATCGT 803
Db 13706 CTTTTCGCGGTTGTTACTGACTGCGACGTAAATCCAGATCTTTTTCGCGTATCGT 13647
QY 804 CTTTTCGCGTCTCAAAACAAACAGCGCGGCGGAAAGTTTTCACCGCGTATCTGCGGAAAG 863
Db 13646 CTTTTCGCGTCTCAAAACAAACAGCGCGGCGGAAAGTTTTCACCGCGTATCTGCGGAAAG 13587
QY 864 ACCTGCGACCTGCTGCGAAGATGTTGGGGTGTGAGCAAGATGAGTTCATTTGAGC 923
Db 13586 ACCTGCGACCTGCTGCGAAGATGTTGGGGTGTGAGCAAGATGAGTTCATTTGAGC 13527
QY 924 GGGAGCCACCTGATAGCTTTGTAATTATCAGAGCTTCAGGCGGTCAACGATGAAGAA 983
Db 13526 GGGAGCCACCTGATAGCTTTGTAATTATCAGAGCTTCAGGCGGTCAACGATGAAGAA 13467
QY 984 GTGTGCTTTCGTCGCAAGTAACTATGTCCTCGAATGTAAAGCATTCATCTTTGCAAT 1043

Db 13466 GTGTGCTTTCGTCGCAAGTAACTATGTCCTCGAATGTAAAGCATTCATCTTTGCAAT 13407
QY 1044 CAAGGCGTTGCTGCTCCGAGATTGTTTACATTAACCGACATATATAGACCTCTCAC 1103
Db 13406 CAAGGCGTTGCTGCTCCGAGATTGTTTACATTAACCGACATATATAGACCTCTCAC 13347
QY 1104 ACAAGTTCGCTCTTTGATTAAGCCGACGCTTTTCCGGTATCCAGATCCAAACCTT 1163
Db 13346 ACAAGTTCGCTCTTTGATTAAGCCGACGCTTTTCCGGTATCCAGATCCAAACCTT 13287
QY 1164 CGCTTCAAAAATAGAAACAACTTACCGACCGGCGCGGTTTATCATCCGCCCTGGGTGT 1223
Db 13286 CGCTTCAAAAATAGAAACAACTTACCGACCGGCGCGGTTTATCATCCGCCCTGGGTGT 13227
QY 1224 AATCAGAAATAGCTGATAGTCTCAGTAGCCCATATCTTGGCTGATACCTGCGAGATG 1283
Db 13226 AATCAGAAATAGCTGATAGTCTCAGTAGCCCATATCTTGGCTGATACCTGCGAGATG 13167
QY 1284 GAACTCTTGGCAAACGCTTCCCGCATCTTCTTGAAGAGGAGGCGCCACAGAACCAAT 1343
Db 13166 GAACTCTTGGCAAACGCTTCCCGCATCTTCTTGAAGAGGAGGCGCCACAGAACCAAT 13107
QY 1344 TTGCTGTAATTAAGTAAATCGTATTTGTCATACAGATGCTTTGGCGAAGAGAGAA 1403
Db 13106 TTGCTGTAATTAAGTAAATCGTATTTGTCATACAGATGCTTTGGCGAAGAGAGAA 13047
QY 1404 TAGGGTTGCGACGACGAGCGACTTTGAAATCTTGTATCTGTAAGGCTCTCGAAGAACAG 1463
Db 13046 TAGGGTTGCGACGACGAGCGACTTTGAAATCTTGTATCTGTAAGGCTCTCGAAGAACAG 12987
QY 1464 CTCTTCTTCAATCTATATCAATTAAAGCACTCGAATCCACATATCAAAATATCCAGTGT 1523
Db 12986 CTCTTCTTCAATCTATATCAATTAAAGCACTCGAATCCACATATCAAAATATCCAGTGT 12927
QY 1524 AGTAAACATTCGAAACCGGATGAGTAAAGAAACAACTTAAATAGCGATACCGGAAT 1583
Db 12926 AGTAAACATTCGAAACCGGATGAGTAAAGAAACAACTTAAATAGCGATACCGGAAT 12867
QY 1584 GATTGATGCGCAAAATATAGATCTCTGCGATGCGAATCTCACCGCAGGAGTTCTATG 1643
Db 12866 GATTGATGCGCAAAATATAGATCTCTGCGATGCGAATCTCACCGCAGGAGTTCTATG 12807
QY 1644 AGGCAAGCGACACTTTTAGCGACAGCAAGTATCCAGAGAGTTATGATCGATC 1703
Db 12806 AGGCAAGCGACACTTTTAGCGACAGCAAGTATCCAGAGAGTTATGATCGATC 12747
QY 1704 TGTCTTGTCCCTATGCAAGGACCTGCGCAAAATGCTATTCATTAAACCGGGAAGTATG 1763
Db 12746 TGTCTTGTCCCTATGCAAGGACCTGCGCAAAATGCTATTCATTAAACCGGGAAGTATG 12687
QY 1764 ATGAGATGTCAGCAAGCTGTACATCGACTGAATCCCTGATATCCGTTTATGATCCAT 1823
Db 12686 ATGAGATGTCAGCAAGCTGTACATCGACTGAATCCCTGATATCCGTTTATGATCCAT 12627
QY 1824 GATTAATATTTTGGATGATGAGGACTTTTTCGACGCTTCAAAATTTTTCGAAACC 1883
Db 12626 GATTAATATTTTGGATGATGAGGACTTTTTCGACGCTTCAAAATTTTTCGAAACC 12567
QY 1884 CTTTTCGAAACGAAACACAGCTGAGCTGCGGAAATGCGCCATCTTGTAGCAATTCAG 1943
Db 12566 CTTTTCGAAACGAAACACAGCTGAGCTGCGGAAATGCGCCATCTTGTAGCAATTCAG 12507
QY 1944 TTCATTATTAATGTCGTTGCGCGGCGCAACTGCAATCTCCGATTAATTAAGCGCCCAAC 2003
Db 12506 TTCATTATTAATGTCGTTGCGCGGCGCAACTGCAATCTCCGATTAATTAAGCGCCCAAC 12447
QY 2004 CGGCAATTAAGATTAAGAGAGTTTCACTGCAATACAGAGATCTGTGATTTGTATTGAG 2063
Db 12446 CGGCAATTAAGATTAAGAGAGTTTCACTGCAATACAGAGATCTGTGATTTGTATTGAG 12387
QY 2064 CCCATATGCTTTCATAGCTTCTGCGCAACGGAACGACATTTGGAAGTACTCAGCGTAAT 2123

Db 12386 CCCATATGCTTTCATAGCTTCTGCAACCGAAGCAATTTGAGTAAGTCAAGCTAAGT 12327
Qy 2124 GATGTCCACTCGATATGTGTCATCTGTAAAGCAATTTGTTCCAGAACCGAGGCGTAATCT 2183
Db 12326 GATGTCCACTCGATATGTGTCATCTGTAAAGCAATTTGTTCCAGAACCGAGGCGTAATCT 12267
Qy 2184 CTTTCATAGCCTTATGAGTGTCTCTCAGGCGTTCCATCTCCAGGCGATAGAAATGAGCCG 2243
Db 12266 CTTTCATAGCCTTATGAGTGTCTCTCAGGCGTTCCATCTCCAGGCGATAGAAATGAGCCG 12207
Qy 2244 CGGCGCTTCTTATGTTTGTGCGCTTTCATAGGACG 2282
Db 12206 CGGCGCTTCTTATGTTTGTGCGCTTTCATAGGACG 12168

RESULT 9
US-09-577-424-1/c
; Sequence 1, Application US/09577424
; Patent No. 6525245
; GENERAL INFORMATION:
; APPLICANT: Rhodia, David M
; TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
; FILE REFERENCES: UNT2990
; CURRENT APPLICATION NUMBER: US/09/577,424
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 12614
; TYPE: DNA
; ORGANISM: Bacterial Plasmid DNA - Plasmid pZP-ALB
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1665) .. (3317)
US-09-577-424-1

Query Match 59.7%; Score 1653.4; DB 4; Length 12614;
Best Local Similarity 99.9%; Pred. No. 9..2e-303;
Matches 1654; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 624 TTAAAGGAGGATTTCCGCGCTTCTTGGCTTATGAGGATCTCTGATTTTCTTGC 683
Db 3317 TTAAAGGAGGATTTCCGCGCTTCTTGGCTTATGAGGATCTCTGATTTTCTTGC 3258
Qy 684 GTGAGTTTTCGGAAGAAGCTTTCGTAATCTGTGCACAAACAACTCTCCGCGAA 743
Db 3257 GTGAGTTTTCGGAAGAAGCTTTCGTAATCTGTGCACAAACAACTCTCCGCGAA 3198
Qy 744 CTTTTCGCGGTTTACTGATGCTGCGAGCTAATCCAGATCTCTTTTCCGTATCGT 803
Db 3197 CTTTTCGCGGTTTACTGATGCTGCGAGCTAATCCAGATCTCTTTTCCGTATCGT 3138
Qy 804 CTTTTCGCTCCAAACAAACAGCGCGGGAAGTTCAACGCGGCTATCGTCGGGAAG 863
Db 3137 CTTTTCGCTCCAAACAAACAGCGCGGGAAGTTCAACGCGGCTATCGTCGGGAAG 3078
Qy 864 ACCTGAGACACTGCTGCAAGATGTTGGGTTGAGAGCAAGATGATTCATTCACG 923
Db 3077 ACCTGAGACACTGCTGCAAGATGTTGGGTTGAGAGCAAGATGATTCATTCACG 3018
Qy 924 GGGAGCCACTGATAGCTTGTATCTTAATCAGACCTTCAAGCGGCTCAACGATGAAGAA 983
Db 3017 GGGAGCCACTGATAGCTTGTATCTTAATCAGACCTTCAAGCGGCTCAACGATGAAGAA 2958
Qy 984 GGTTCGTCTGCTCCAGATGCTAATCTCAGATGATGACATCAATCTTCAT 1043
Db 2957 GGTTCGTCTGCTCCAGATGCTAATCTCAGATGATGACATCAATCTTCAT 2898
Qy 1044 CAAGCGTTGATGCTTCCGATTTGTTATACATACCGGACATATATAGACCTCTCAC 1103
Db 2897 CAAGCGTTGATGCTTCCGATTTGTTATACATACCGGACATATATAGACCTCTCAC 2838

Qy 1104 ACACAGTTGCGCTTTTGATTAACCGCCAGCGCTTTCCCGGATATCCAGATCCAACTT 1163
Db 2837 ACACAGTTGCGCTTTTGATTAACCGCCAGCGCTTTCCCGGATATCCAGATCCAACTT 2778
Qy 1164 CGCTTCAAAAAATGAAACAATTTTACCGACCGGCGCGGTTTATATCCCTCGGGTGT 1223
Db 2777 CGCTTCAAAAAATGAAACAATTTTACCGACCGGCGCGGTTTATATCCCTCGGGTGT 2718
Qy 1224 AATCAGAAATGCTGATATGTTCTCAGTGAAGCCCATATCTTTCGCTGATCTCTGAGAA 1283
Db 2717 AATCAGAAATGCTGATATGTTCTCAGTGAAGCCCATATCTTTCGCTGATCTCTGAGAA 2658
Qy 1284 GAACCTCTGGCAACGCTTCCCGACCTTCTTGAAGAGGAGGCGCCACGAAAGCAAT 1343
Db 2657 GAACCTCTGGCAACGCTTCCCGACCTTCTTGAAGAGGAGGCGCCACGAAAGCAAT 2598
Qy 1344 TTGCTGTAATTAATGATTAATCGTATTTGTCAATCAGAGTCTTTTGGCAGAGAGAA 1403
Db 2597 TTGCTGTAATTAATGATTAATCGTATTTGTCAATCAGAGTCTTTTGGCAGAGAGAA 2538
Qy 1404 TAGGTTGGACACGACGCGCACTTTGAATCTTGTATCTCTGAAGGCTCTCGAAACAG 1463
Db 2537 TAGGTTGGACACGACGCGCACTTTGAATCTTGTATCTCTGAAGGCTCTCGAAACAG 2478
Qy 1464 CTCTTCTTCAATCTATACATTAAGACGACTGAAATCCACATATCAATATCCGAGTGT 1523
Db 2477 CTCTTCTTCAATCTATACATTAAGACGACTGAAATCCACATATCAATATCCGAGTGT 2418
Qy 1524 AGTAAACATTCGAAACCGTGTATGATGAATGAACAACATTTAAATCGAGATCCGGAAT 1583
Db 2417 AGTAAACATTCGAAACCGTGTATGATGAATGAACAACATTTAAATCGAGATCCGGAAT 2358
Qy 1584 GATTTGATTCGCAAAATATGATCTCTGCGATGCGAATCTCAGCGGCGCTTATG 1643
Db 2357 GATTTGATTCGCAAAATATGATCTCTGCGATGCGAATCTCAGCGGCGCTTATG 2298
Qy 1644 AGGCAAGCGGACCTTTAGAGAGCCAGTATATCCAGAGGTTCAATGATGCAAT 1703
Db 2297 AGGCAAGCGGACCTTTAGAGAGCCAGTATATCCAGAGGTTCAATGATGCAAT 2238
Qy 1704 TGTCTTGTCCCTATGGAAGACTCTGSCAAATATGATTAATTAACCGGAGGTAG 1763
Db 2237 TGTCTTGTCCCTATGGAAGACTCTGSCAAATATGATTAATTAACCGGAGGTAG 2178
Qy 1764 ATGAGATGAGCAACGTTATGATGACTGAATCCCTGTATATCCGTTTGAATCAT 1823
Db 2177 ATGAGATGAGCAACGTTATGATGACTGAATCCCTGTATATCCGTTTGAATCAT 2118
Qy 1824 GATTAATTAATTTTGTGATGATGAGAGCTTTTGTGACGTTCAAAATTTTGTGAACCC 1883
Db 2117 GATTAATTAATTTTGTGATGATGAGAGCTTTTGTGACGTTCAAAATTTTGTGAACCC 2058
Qy 1884 CTTTTCGAAAGCAACACCGGTAGGCTGCGAAATGCCATATCTTGTGAGCAATTCAG 1943
Db 2057 CTTTTCGAAAGCAACACCGGTAGGCTGCGAAATGCCATATCTTGTGAGCAATTCAG 1998
Qy 1944 TTCAATTAATATGTCTGTCGCGGCGCAACTGCAACTCCGATTAATTAACGCGCCCAAC 2003
Db 1997 TTCAATTAATATGTCTGTCGCGGCGCAACTGCAACTCCGATTAATTAACGCGCCCAAC 1938
Qy 2004 CGGCAATTAAGAAATTAAGAGATTTTCACTGATACGAGATTCGTGATTTGTATTCAG 2063
Db 1937 CGGCAATTAAGAAATTAAGAGATTTTCACTGATACGAGATTCGTGATTTGTATTCAG 1878
Qy 2064 CCCATATGCTTATAGCTTCTGCAACGGAATTTGAGATCTCAGCTTAAGT 2123
Db 1877 CCCATATGCTTATAGCTTCTGCAACGGAATTTGAGATCTCAGCTTAAGT 1818
Qy 2124 GATGTCCACTCGATATGTGATCTGTAAAGCAATTTGTTCCAGAACCGAGGCGTATCT 2183
Db 1817 GATGTCCACTCGATATGTGATCTGTAAAGCAATTTGTTCCAGAACCGAGGCGTATCT 1758
Qy 2184 CTTTCATAGCTTATGCAATGTGCTCTCAGCGGTTCCATCTTCCAGCGGATAGAAATGGCGC 2243

Db 1757 CTTATAGCCTTATGACAGTCTCTCCAGCGGCTTCATCTTCAGCGGATGAGATGCGC 1698
Qy 2244 CGGGCCTTCTTTATGATTTTGGGCTCTTCATGG 2278
Db 1697 CGGGCCTTCTTTATGATTTTGGGCTCTTCATGG 1663

RESULT 10
US-09-743-194-19/c
; Sequence 19, Application US/09743194
; Patent No. 6716601
; GENERAL INFORMATION:
; APPLICANT: Bellfield, Graham
; APPLICANT: Oakley, Caroline
; TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
; FILE REFERENCE: 3526, 82543
; CURRENT APPLICATION NUMBER: US/09/743,194
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 12844
; TYPE: DNA
; ORGANISM: *Saccharomyces cerevisiae*
US-09-743-194-19

Query Match 59.6%; Score 1651.4; DB 4; Length 12844;
Best Local Similarity 99.9%; Pred. No. 2,2e-302;
Matches 1652; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 624 TTAACGGCGCATCTTTCGCGCCTTCTGGCCTTATGAGATCTCTGATTTTCTTGC 683
Db 2162 TTACAGCGGCATCTTTCGCGCCTTCTGGCCTTATGAGATCTCTGATTTTCTTGC 2103
Qy 684 GTGAGTTTCCGATGAAGCCTTTCGGTACTTGTCCAAACAACTCTCCGCGCAA 743
Db 2102 GTGAGTTTCCGATGAAGCCTTTCGGTACTTGTCCAAACAACTCTCCGCGCAA 2043
Qy 744 CTTTTCGGCGGTGTATCTTGAATGAGGATTCACAGATCTCTTTCGGTCAAT 803
Db 2042 CTTTTCGGCGGTGTATCTTGAATGAGGATTCACAGATCTCTTTCGGTCAAT 1883
Qy 804 CTTTTCGGCTCCAAACAAACGAGCGGCGGAAAGTTCAACCGCGCTCATGTCGGAAG 863
Db 1982 CTTTTCGGCTCCAAACAAACGAGCGGCGGAAAGTTCAACCGCGCTCATGTCGGAAG 1923
Qy 864 ACCTGACACCTGCGTGAAGATGTTGGGCTGTGGAGCAATGATTCATTCAGC 923
Db 1922 ACCTGACACCTGCGTGAAGATGTTGGGCTGTGGAGCAATGATTCATTCAGC 1863
Qy 924 GGGAGCACTGATAGGCTTTTATCTTAATCAGAGATCTTTCGGGCTCAACATGAAGA 983
Db 1862 GGGAGCACTGATAGGCTTTTATCTTAATCAGAGATCTTTCGGGCTCAACATGAAGA 1803
Qy 984 GTGTCTCTCTGCTCCAGTAAAGTATGTCAGATGAGCATTCATCTTGTCAAT 1043
Db 1802 GTGTCTCTCTGCTCCAGTAAAGTATGTCAGATGAGCATTCATCTTGTCAAT 1743
Qy 1044 CAAGGCTGTGCTCCGATTTGTTACATAACCGGACATATCATAGAGCTCTCAC 1103
Db 1742 CAAGGCTGTGCTCCGATTTGTTACATAACCGGACATATCATAGAGCTCTCAC 1083
Qy 1104 ACAAGTTCGCTCTTCTTGAATTAAGCCAGGCTTTTCCGGTATCCAGATCCAACTT 1163
Db 1682 ACAAGTTCGCTCTTCTTGAATTAAGCCAGGCTTTTCCGGTATCCAGATCCAACTT 1623
Qy 1164 CGCTTCAAAAATGGAACAATTACAGACGCGCGGCTTATCATCCCTCGGGTGT 1223
Db 1622 CGCTTCAAAAATGGAACAATTACAGACGCGCGGCTTATCATCCCTCGGGTGT 1563
Qy 1224 AATCAGAAATGCTGATGATCTCAGTGAAGCCCATATCTTGCCTGATACCTGAGATG 1283

Db 1562 AATCAGAAATGCTGATGATCTCAGTGAAGCCCATATCTTGCCTGATACCTGAGATG 1503
Qy 1284 GAACCTTTTGGCAACCGCTTCCCGACTTCTTATGAGAGGGAGCGCCACCAAGCAAT 1343
Db 1502 GAACCTTTTGGCAACCGCTTCCCGACTTCTTATGAGAGGGAGCGCCACCAAGCAAT 1443
Qy 1344 TTCGTAAATTTGATTAATGATTTGTCAATCAGATGCTTTTGGCAAGAGAGA 1403
Db 1442 TTCGTAAATTTGATTAATGATTTGTCAATCAGATGCTTTTGGCAAGAGAGA 1383
Qy 1404 TAGGTTGGACAGACGCGCACTTGAATCTTGTAACTGAAAGCTCTCGAAGACAG 1463
Db 1382 TAGGTTGGACAGACGCGCACTTGAATCTTGTAACTGAAAGCTCTCGAAGACAG 1323
Qy 1464 CTCTTCTTCAAACTTATGATTTAAAGAGCTGAAATCCCAATTAATATCCGAGTGT 1523
Db 1322 CTCTTCTTCAAACTTATGATTTAAAGAGCTGAAATCCCAATTAATATCCGAGTGT 1263
Qy 1524 AGTAAACATTCAAAAACCGTATGATGAATGAACAACTTAAATCGAGTATCCGGAAT 1583
Db 1262 AGTAAACATTCAAAAACCGTATGATGAATGAACAACTTAAATCGAGTATCCGGAAT 1203
Qy 1584 GATTTGATTCGCAAAAATAGATCTCTGCGATGCGAATCTTCAAGCAGGCACTTATG 1643
Db 1202 GATTTGATTCGCAAAAATAGATCTCTGCGATGCGAATCTTCAAGCAGGCACTTATG 1143
Qy 1644 AGGCAAGGCAACCTTTAGGCGAGACAGTATGATCCAGAGAGTTATGATGTCAT 1703
Db 1142 AGGCAAGGCAACCTTTAGGCGAGACAGTATGATCCAGAGAGTTATGATGTCAT 1083
Qy 1704 TGTCTTCCCTTTCGAAAGACTCTGCGCAAAAATGATTTCAATTAACCGGGAAGTATG 1763
Db 1082 TGTCTTCCCTTTCGAAAGACTCTGCGCAAAAATGATTTCAATTAACCGGGAAGTATG 1023
Qy 1764 ATGAGATGAGCAAGAGTGTATCTGACTGAATCCCTGATATCCGTTTATGAATCAT 1823
Db 1022 ATGAGATGAGCAAGAGTGTATCTGACTGAATCCCTGATATCCGTTTATGAATCAT 963
Qy 1824 GATTAATATTTTGGATGATTTGGAGCTTTTTCGAGTTCAAAATTTTTCGAACCC 1883
Db 962 GATTAATATTTTGGATGATTTGGAGCTTTTTCGAGTTCAAAATTTTTCGAACCC 903
Qy 1884 CTTTTCGAAACGAACCAACGCTAGCTGCGAAATGCCATATCTGAGCAATTCAGC 1943
Db 902 CTTTTCGAAACGAACCAACGCTAGCTGCGAAATGCCATATCTGAGCAATTCAGC 843
Qy 1944 TTCAATTAATATGCTGCTGCGGCGCAACTGCAACTCCGATTAATTAAGCGGCCAAGC 2003
Db 842 TTCAATTAATATGCTGCTGCGGCGCAACTGCAACTCCGATTAATTAAGCGGCCAAGC 783
Qy 2004 CGGCAATTAAGATTAAGAGATTTTCACTGATAGAGATTTCTGTGATTTGATTCAG 2063
Db 782 CGGCAATTAAGATTAAGAGATTTTCACTGATAGAGATTTCTGTGATTTGATTCAG 723
Qy 2064 CCCATATGCTTCAATATGCTTTCGCAACCGAAGCACTTTCGAAAGTATCAAGCGTAACT 2123
Db 722 CCCATATGCTTCAATATGCTTTCGCAACCGAAGCACTTTCGAAAGTATCAAGCGTAACT 663
Qy 2124 GATGTCACCTGATATGATCTGTAAAGCAATTTTTCAGAGAACCAAGGCGATATCT 2183
Db 662 GATGTCACCTGATATGATCTGTAAAGCAATTTTTCAGAGAACCAAGGCGATATCT 603
Qy 2184 CTTCAATAGCTTATGAGATTTCTTCAGCGGTTTCATTTCCAGCGGATTAATAGGCGC 2243
Db 602 CTTCAATAGCTTATGAGATTTCTTCAGCGGTTTCATTTCCAGCGGATTAATAGGCGC 543
Qy 2244 CGGGCCTTCTTATGATTTTGGCGTCTTCAT 2276
Db 542 CGGGCCTTCTTATGATTTTGGCGTCTTCAT 510

RESULT 11


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US-09-743-194-20/c
: Sequence 20, Application US/09743194
: Patent No. 6716601
:
: GENERAL INFORMATION:
:
: APPLICANT: Bellfield, Graham
:
: TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
:
: TITLE OF INVENTION: Controlling Nucleic Acid Expression in Yeast
:
: FILE REFERENCE: 3526.82543
:
: CURRENT APPLICATION NUMBER: US/09/743,194
:
: CURRENT FILING DATE: 2001-01-08
:
: NUMBER OF SEQ ID NOS: 32
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 20
:
: LENGTH: 13073
:
: TYPE: DNA
:
: ORGANISM: Saccharomyces cerevisiae
:
: US-09-743-194-20

```

| | | | | |
|----------------------------|--------|---------------------|-----------|---------------|
| Query Match | 59.6% | Score 1651.4; | DB 4; | Length 13073; |
| Best Local Similarity | 99.0%; | Pred. No. 2.2e-302; | | |
| Matches 1661; Conservative | 0; | Mismatches 16; | Indels 0; | Gaps 0; |

| | | | |
|----|------|--|------|
| QY | 624 | TTAAACGGCGANCTTTCCGCCCTTCGAGCCCTTAATGAGANCTCTGATTTTTCTTGC | 683 |
| Db | 2391 | TTACACGGCGANCTTTCCGCCCTTCGAGCCCTTAATGAGANCTCTGATTTTTCTTGC | 2332 |
| QY | 684 | GTGAGTGTTCGCGTAAGACCTTTCGTAATCTGTCGTCACAAACAACTCTCCGCGCA | 743 |
| Db | 2331 | GTGAGTGTTCGCGTAAGACCTTTCGTAATCTGTCGTCACAAACAACTCTCCGCGCA | 2272 |
| QY | 744 | CTTTTTGGCGGTGTTAATTGACTGAGCGACGTATCCAGATCTCTTTTTCCGTATGT | 803 |
| Db | 2271 | CTTTTTGGCGGTGTGTACTTGACTGAGCGACGTAAATCCAGATCTCTTTTTCCGTATGT | 2212 |
| QY | 804 | CTTTCGCGGTCTCCAAAACAACACGGCGCGGGAAGTTCAACGGCGGTATCGTCGGAA | 863 |
| Db | 2211 | CTTTCGCGGTCTCCAAAACAACACGGCGCGGGAAGTTCAACGGCGGTATCGTCGGAA | 2153 |
| QY | 864 | ACTGCGACACTCGTCGTGAAAGATGTTGGGTGTTGANGACAAGATGATTCATTCAC | 923 |
| Db | 2151 | ACTGCGACACTCGTCGTGAAAGATGTTGGGTGTTGANGACAAGATGATTCATTCAC | 2092 |
| QY | 924 | GGGAGCAACCTGATAGCCTTTGTACTTAATAGAGACTTCAGCGCGTCAAGATGAAGAA | 983 |
| Db | 2091 | GGGAGCAACCTGATAGCCTTTGTACTTAATAGAGACTTCAGCGCGTCAAGATGAAGAA | 2032 |
| QY | 984 | GTGTTCGCTTCGTCCAGTAAGCATGTCTCCAGAAATGTAAGCATCCATCCTTGTCAAT | 1043 |
| Db | 2031 | GTGTTCGCTTCGTCCAGTAAGCATGTCTCTCCAGAAATGTAAGCATCCATCCTTGTCAAT | 1972 |
| QY | 1044 | CAAGCGGTGGTCGCTTCGGAATGTTTACATTAACCGGACATTAATCATAGGACCTTCAC | 1103 |
| Db | 1971 | CAAGCGGTGGTCGCTTCGGAATGTTTACATTAACCGGACATTAATCATAGGACCTTCAC | 1912 |
| QY | 1104 | ACAGAGTTGCGCTCTTGAATTAAGCCACGAGTTTCCCGGTATCCANATCACAACCTT | 1163 |
| Db | 1911 | ACAGAGTTGCGCTCTTGAATTAAGCCACGAGGTTTTCCCGGTATCCANATCACAACCTT | 1852 |
| QY | 1164 | CGCTTCAAAAAATGGAACAATTAAACGACCGCGCCGGTTTATCATCCCTCGGAGT | 1223 |
| Db | 1851 | CGCTTCAAAAAATGGAACAATTAAACGACCGCGCGGTTTATCATCCCTCGGAGT | 1792 |
| QY | 1224 | AATCAGAAATAGCTGATGTATGTCTAGTGAAGCCCATATCTTGGCTGATACCTGCGCAN | 1283 |
| Db | 1791 | AATCAGAAATAGCTGATGTATGTCTAGTGAAGCCCATATCTTGGCTGATACCTGCGCAN | 1732 |
| QY | 1284 | GAACTCTTGGCAACCGCTTCCCGCATCTTCTTAAGAGAGGAGGCGCACAGAAACAT | 1343 |
| Db | 1731 | GAACTCTTGGCAACCGCTTCCCGCATCTTCTTAAGAGAGGAGGCGCACAGAAACAT | 1672 |
| QY | 1344 | TTGCTGTAATTAAGTAATAATGTAATTTGTCAATCAGAGTCTTTTGGCAAGAAAGAA | 1403 |

| | | | |
|---|------|---|------|
| Dd | 1671 | TTGCTGTAAATTAATATAATTCGTATTTTGTCATTCAGAGTGGCTTTTGGCGAAGAAGAGGAA | 1612 |
| Qy | 1404 | TAGGGTTGGCCACGACAGCGCATCTTGAATCTGTAAATCTGAAAGCTCCTCAGAAA | 1463 |
| Dd | 1611 | TAGGGTTGGCCACGACAGCGCATCTTGAATCTGTAAATCTGAAAGCTCCTCAGAAA | 1552 |
| Qy | 1464 | CTCTTTTCCAAATCTATATCAATTAAGACGACTCCGAAATCCCATATTCAAATATCCGACGT | 1523 |
| Dd | 1551 | CTCTTTTCCAAATCTATATCAATTAAGACGACTCCGAAATCCCATATTCAAATATCCGACGT | 1492 |
| Qy | 1524 | AGTAAACATTCCAAACCCGATATGGATATGGAAACAACACTTAAATCCGATATCCGAAAT | 1583 |
| Dd | 1491 | AGTAAACATTCCAAACCCGATATGGATATGGAAACAACACTTAAATCCGATATCCGAAAT | 1432 |
| Qy | 1584 | GATTTGATTTGCGCAAAAATAGGATCTCTGGCATGCGAATCTCAACGAGCGATTTATG | 1643 |
| Dd | 1431 | GATTTGATTTGCGCAAAAATAGGATCTCTGGCATGCGAATCTCAACGAGCGATTTATG | 1372 |
| Qy | 1644 | AGGCAAGCGCACACTTTTAGGCGACACAGTATGATTCAGAGAGTTCAATGATCAATGCAAT | 1703 |
| Dd | 1371 | AGGCAAGCGCACACTTTTAGGCGACACAGTATGATTCAGAGAGTTCAATGATCAATGCAAT | 1312 |
| Qy | 1704 | TGCTTTGGCCCTATCGAAGGACCTGGCAAAAATCGATATTCATTAACCCGGAGGTAG | 1763 |
| Dd | 1311 | TGCTTTGGCCCTATCGAAGGACCTGGCAAAAATCGATATTCATTAACCCGGAGGTAG | 1252 |
| Qy | 1764 | ATGAGATGTGACGAACGCTGTACATCGACTGAATATCCCTGGTAAATCCGTTTATGAAATCAT | 1823 |
| Dd | 1251 | ATGAGATGTGACGAACGCTGTACATCGACTGAATATCCCTGGTAAATCCGTTTATGAAATCAT | 1192 |
| Qy | 1824 | GATATATATTTTTTGGATGATTTGGGAGCTTTTTTGCACGTTCAAAAATTTTTTGCAACC | 1883 |
| Dd | 1191 | GATATATATTTTTTGGATGATTTGGGAGCTTTTTTGCACGTTCAAAAATTTTTTGCAACC | 1132 |
| Qy | 1884 | CTTTTTGAAAACGAACCAACGCGTAGGCTCGGAAATGCCCCATCTGTGTAGCAATTACG | 1943 |
| Dd | 1131 | CTTTTTGAAAACGAACCAACGCGTAGGCTCGGAAATGCCCCATCTGTGTAGCAATTACG | 1072 |
| Qy | 1944 | TTTCATTTAAATGTCGTTCCGCGGCGCGCACTGCACATCCGATAAATTAACCGGCCCAACAC | 2003 |
| Dd | 1071 | TTTCATTTAAATGTCGTTCCGCGGCGCGCACTGCACATCCGATAAATTAACCGGCCCAACAC | 1012 |
| Qy | 2004 | CGGCATAAAGAAATGAAGAAGATTTTCACTGCATACGACGATTTCTGTGATTTGATTCAG | 2063 |
| Dd | 1011 | CGGCATAAAGAAATGAAGAAGATTTTCACTGCATACGACGATTTCTGTGATTTGATTCAG | 952 |
| Qy | 2064 | CCCATATTCGTTTCACTACCTTCTGCAACCGAACGGACATTTTCGAAGTACTCAGGTAACT | 2123 |
| Dd | 951 | CCCATATTCGTTTCACTACCTTCTGCAACCGAACGGACATTTTCGAAGTACTCAGGTAACT | 892 |
| Qy | 2124 | GATGTCCACCTCGATATGTGATCTGTAAAGCAATTTGTTCCAGGAACACAGGGCGTATCT | 2183 |
| Dd | 891 | GATGTCCACCTCGATATGTGATCTGTAAAGCAATTTGTTCCAGGAACACAGGGCGTATCT | 832 |
| Qy | 2184 | CTTCATAGCCTTATGACAGTTGCTCTCCAGCGGTTTCCATCTTCCAGCGGATAGATGCGC | 2243 |
| Dd | 831 | CTTCATAGCCTTATGACAGTTGCTCTCCAGCGGTTTCCATCTTCCAGCGGATAGATGCGC | 772 |
| Qy | 2244 | CGGGCCTTTTCTTATATGTTTTTGGGCGCTTTCATATGGAACGTCGGTGTGTTTACGTT | 2300 |
| Dd | 771 | CGGGCCTTTTCTTATATGTTTTTGGGCGCTTTCATATATGTTATATGATCTTTTTTTTT | 715 |
| | | | |
| RESUB. 12 | | | |
| US-08-354-240A-3/c | | | |
| ; Sequence 3, Application US/08354240A | | | |
| ; Patent No. 5670356 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Sherf, Bruce A. | | | |
| ; APPLICANT: Wood, Keith V. | | | |
| ; TITLE OF INVENTION: MODIFIED LUCIFERASE | | | |
| ; NUMBER OF SEQUENCES: 20 | | | |
| ; CORRESPONDENCE ADDRESS: | | | |

RESULT 12
US-08-354-240A-3/C
; Sequence 3, Application US/08354240A
; Patent No. 5670356
; GENERAL INFORMATION:
; APPLICANT: Sherf, Bruce A.
; APPLICANT: Wood, Keith V.
; TITLE OF INVENTION: MODIFIED LUCIFERASE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:

```

: ADDRESSEE: Demilt Ross & Stevens, S.C.
: STREET: 8000 Excelstior Drive, Suite 401
: CITY: Madison
: STATE: WI
: COUNTRY: USA
: ZIP: 53717-1914
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PC-DOS/MS-DOS
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/354,240A
: FILING DATE: 12-DEC-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sara, Charles S.
: REGISTRATION NUMBER: 30,492
: REFERENCE/DOCKET NUMBER: 34506.029
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 608-831-2100
: TELEFAX: 608-831-2106
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1650 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FRAGMENT TYPE: C-terminal
: ORIGINAL SOURCE:
: ORGANISM: Photinus pyralis
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1651
: US-08-354-240A-3

Query Match      59.5%; Score 1649; DB 1; Length 1650;
Best Local Similarity 100.0%; Pred. No. 4e-302;
Matches 1649; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 628 ACGGCGATCTTTCGCGCCCTTCTTGCGCTTATGAGATCTCTGATTTTCTTGCCTG 687
DB 1649 ACGGCGATCTTTCGCGCCCTTCTTGCGCTTATGAGATCTCTGATTTTCTTGCCTG 1590
QY 688 AGTTTTCGGTAAGACCTTTTCGTAATCTTCCCAACAAACAACTCTCCGCGCAATTT 747
DB 1589 AGTTTTCGGTAAGACCTTTTCGTAATCTTCCCAACAAACAACTCTCCGCGCAATTT 1530
QY 748 TTGCGGTTGTTACTTGACTGGGAGGTAATCCAGATCTCTTTTCCGTCATCGTCTT 807
DB 1529 TTGCGGTTGTTACTTGACTGGGAGGTAATCCAGATCTCTTTTCCGTCATCGTCTT 1470
QY 808 CCGTGCTCCAAAACAAACAAACGCGCGCGGAAAGTTCAACCGCGTCATCGTCGGAAGACT 867
DB 1469 CCGTGCTCCAAAACAAACAAACGCGCGCGGAAAGTTCAACCGCGTCATCGTCGGAAGACT 1410
QY 868 GCGACACTGCGCTGCAAGATGTTGGGTTGTTGACAAAGTGAATTCGAATTCAGCGGGA 927
DB 1409 GCGACACTGCGCTGCAAGATGTTGGGTTGTTGACAAAGTGAATTCGAATTCAGCGGGA 1350
QY 928 GCCACCTGATAGCCTTTGTAATTATGAGAGCTTCAGGCGGTCAAGATGAAGAAGTGT 987
DB 1349 GCCACCTGATAGCCTTTGTAATTATGAGAGCTTCAGGCGGTCAAGATGAAGAAGTGT 1290
QY 988 TCGTCTTCTGTCAGTAAGCTATGTCACAGAAATGTAAGCATTCATCTTGTCAATCAAG 1047
DB 1289 TCGTCTTCTGTCAGTAAGCTATGTCACAGAAATGTAAGCATTCATCTTGTCAATCAAG 1230
QY 1048 GCGTTGATCGCTTCGGAATGTTTACATAACCGGACATAATCATAGGACCTTCAACAC 1107
DB 1229 GCGTTGATCGCTTCGGAATGTTTACATAACCGGACATAATCATAGGACCTTCAACAC 1170
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QY 1108 AGTTGCGCTCTTGATTAAGCCGAGGTTTTCGCGGTATCCAGATCCAACTTCGCT 1167
DB 1169 AGTTGCGCTCTTGATTAAGCCGAGGTTTTCGCGGTATCCAGATCCAACTTCGCT 1110
QY 1168 TCAAAAATGGAACAATTACCGACCGCGCGGTTTATCATCTCCCTCGGTTAATC 1227
DB 1109 TCAAAAATGGAACAATTACCGACCGCGCGGTTTATCATCTCCCTCGGTTAATC 1050
QY 1228 AGAATAGCTGATGATCTTCAGTGAAGCCATATCTTGGCTGATTAATCTGCAATGGAAC 1287
DB 1049 AGAATAGCTGATGATCTTCAGTGAAGCCATATCTTGGCTGATTAATCTGCAATGGAAC 990
QY 1288 CTCTTGGCAACCGCTTCCCGACTTCCTTGAAGAGGAGCGCCACAGAAAGCAATTCG 1347
DB 989 CTCTTGGCAACCGCTTCCCGACTTCCTTGAAGAGGAGCGCCACAGAAAGCAATTCG 930
QY 1348 TGTAAATTAATTAATGATGTAATTTGTCAATCAGAGTCTTTTGGCGAAGAGGAATAGG 1407
DB 929 TGTAAATTAATTAATGATGTAATTTGTCAATCAGAGTCTTTTGGCGAAGAGGAATAGG 870
QY 1408 GTTGGCACCAAGCGGCACTTTGAAATCTTGTAATCTCTGAAGGTCCTTCAGAAACACTCT 1467
DB 869 GTTGGCACCAAGCGGCACTTTGAAATCTTGTAATCTCTGAAGGTCCTTCAGAAACACTCT 810
QY 1468 TCTTCAAAATCTATACATTAAGACACTCGAAATCCACATATCAAAATATCCGAGTATGA 1527
DB 809 TCTTCAAAATCTATACATTAAGACACTCGAAATCCACATATCAAAATATCCGAGTATGA 750
QY 1528 AACATTCAAAACCGGATGGAATGGAACAACTTAAATCGCACTATCCGGAATGAT 1587
DB 749 AACATTCAAAACCGGATGGAATGGAACAACTTAAATCGCACTATCCGGAATGAT 690
QY 1588 TGAATTCGCAAAAATAGGATCTCTGGCATCGGAAATCTCAACGAGGCACTCTATAGGC 1647
DB 689 TGAATTCGCAAAAATAGGATCTCTGGCATCGGAAATCTCAACGAGGCACTCTATAGGC 630
QY 1648 AGAGCAGACACTTTAGGACGAGACGATAGATCCAGAGAGTTCATGATCAAGTGAATGTC 1707
DB 629 AGAGCAGACACTTTAGGACGAGACGATAGATCCAGAGAGTTCATGATCAAGTGAATGTC 570
QY 1708 TTGTCCCTATCGAAGGACTCTGGCAAAAATCGTATTCATTAACCGGAGGTAGATGA 1767
DB 569 TTGTCCCTATCGAAGGACTCTGGCAAAAATCGTATTCATTAACCGGAGGTAGATGA 510
QY 1768 GATGTACGAAAGCTGTACATCCAGTGAATCCCTGTAATCCGTTTAAATTCATGATA 1827
DB 509 GATGTACGAAAGCTGTACATCCAGTGAATCCCTGTAATCCGTTTAAATTCATGATA 450
QY 1828 ATAAATTTTGGATGATGTTGGAGCTTTTGTGACGTTCAAAAATTTTGGCAACCCCTT 1887
DB 449 ATAAATTTTGGATGATGTTGGAGCTTTTGTGACGTTCAAAAATTTTGGCAACCCCTT 390
QY 1888 TTGGAACGAAACACACGAGTGGCTGCGAATGCCATATCTGTAGCAATTCAGCTTGA 1947
DB 389 TTGGAACGAAACACACGAGTGGCTGCGAATGCCATATCTGTGTGCAATTCAGCTTGA 330
QY 1948 TTATAATGTCGTTCCGCGGCGCAATCTGCACTCCGATTAATTAACGCGCCCAACCGGC 2007
DB 329 TTATAATGTCGTTCCGCGGCGCAATCTGCACTCCGATTAATTAACGCGCCCAACCGGC 270
QY 2008 ATTAAGATTTGAAGAGTCTTCACTGCAATGAGAGATCTGTGATTTGATTCAGCCCA 2067
DB 269 ATTAAGATTTGAAGAGTCTTCACTGCAATGAGAGATCTGTGATTTGATTCAGCCCA 210
QY 2068 TATGTTTATAGCTTCTGCAACCGAAGGACATTCGAAATCTCAAGCTATGATGATG 2127
DB 209 TATGTTTATAGCTTCTGCAACCGAAGGACATTCGAAATCTCAAGCTATGATGATG 150
QY 2128 TCGACCTCGATATGTCATCTGTAAGAGCAATTTGTTCCAGAAACCAAGGCGATATCTTTC 2187
DB 149 TCGACCTCGATATGTCATCTGTAAGAGCAATTTGTTCCAGAAACCAAGGCGATATCTTTC 90
QY 2188 ATAGCTTATGAGATGCTCTCAAGCGGTTCCATCTTCAAGGAGATGAATGAGCGCGG 2247
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D_b

89 ATAGCCTTAGCAATTGCTGTCCAGCGGTTCCAATCTTCCAGCGGATGGANTGGCGCCGGG 30

Qy

2248 CCTTCCTTAAGTTTTTGCGCATCTTCCAT 2276

D_b

29 CCTTTCCTTAAGTTTTTGCGCATCTTCCAT 1

RESULT 13
US-09-602

```

US-09-602-628-3/c
Sequence 3, Application US/09602628
Patent No. 6495355
GENERAL INFORMATION:
APPLICANT: Eames, Brian
APPLICANT: Contag, Christopher
TITLE OF INVENTION: Red-Shifted Luciferase
FILE REFERENCE: SUN-127
CURRENT APPLICATION NUMBER: US/09/602,628
CURRENT FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/140,598
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1686
Type: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: red-shifted luciferase mutation
NAME/KEY: CDS
LOCATION: (1) ...(1650)
OTHER INFORMATION: Coding sequence of Clone 1
US-09-602-628-3

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| | | | | |
|----------------------------|-------|--------------------|----------|-------------|
| Query Match | 59.5% | Score 1647.6 | DB 4 | Length 1686 |
| Best Local Similarity | 98.6% | Pred. No. 7.4e-302 | | |
| Matches 1662; Conservative | 0 | Mismatches 24 | Indels 0 | Gaps 0 |

| | | | |
|----|------|---|------|
| QY | 591 | TGGGCTAAGAGAGCCGGAGATGTTAACCCCAACCTTTAAGCGCGATCTTTCGGCCCTTCTT | 650 |
| Db | 1686 | TGCTCGAAGCGGCGCGCGCCCGCACTCTGAATTATACAGGCGAGCTTTCGGCCCTTCTT | 1627 |
| QY | 651 | GAGCCTTTATGAGGATCTCTGATTTTCTTGCGTGCAGTTTTCGGATTAAGACCTTTGCG | 710 |
| Db | 1626 | GGCCTTTATGAGGATCTCTGATTTTCTTGCGTGCAGTTTTCGGATTAAGACCTTTGCG | 1567 |
| QY | 711 | TACTTCGTCCACAACACACACTCCCGCAACTTTTCGCGGTGTACTTGACTGGC | 770 |
| Db | 1566 | TACTTCGTCCACAACACACACTCCCGCAACTTTTCGCGGTGTACTTGACTGGC | 1507 |
| QY | 771 | GACGTAATCAACGATCTCTTTTTCGTCATCGTCTTTCGTCGTCACAACACACGCG | 830 |
| Db | 1506 | GACGTAATCAACGATCTCTTTTTCGTCATCGTCTTTCGTCGTCACAACACACGCG | 1447 |
| QY | 831 | GCGCGGAAGTTCAACCGGCTCATCGTCGGGAAGACTGCGACACTGGGTGGAAGATGTT | 890 |
| Db | 1446 | GCGCGGAAGTTCAACCGGCTCATCGTCGGGAAGACTGCGACACTGGGTGGAAGATGTT | 1387 |
| QY | 891 | GGGGTGTGGAGCAAGATGATTTCCAATTACGCGGAGCCGCACTGATAGCCCTTGTACTT | 950 |
| Db | 1386 | GGGGTGTGGAGCAAGATGATTTCCAATTACGCGGAGCCGCACTGATAGCCCTTGTACTT | 1327 |
| QY | 951 | AATCAGAGACTTCAGCGCGGTCAACGATGAAGAAGTTCGTCCTTCGTCACGTAAGCTAT | 1010 |
| Db | 1326 | AATCAGAGACTTCAGCGCGGTCAACGATGAAGAAGTTCGTCCTTCGTCACGTAAGCTAT | 1267 |
| QY | 1011 | GTCCTCAGATGTAGCCATTCATCTTGTCAATCAAGCGTGTGGTCGCTTCGGAATGTT | 1070 |
| Db | 1266 | GTCCTCAGATGTAGCCATTCATCTTGTCAATCAAGCGTGTGGTCGCTTCGGAATGTT | 1207 |
| QY | 1071 | TACATTAACCGGACATATCATATAGACCTTCAACACAGTTTCGCTCTTTATTTAAGCC | 1130 |
| Db | 1206 | TACATTAACCGGACATATCATATAGACCTTCAACACAGTTTCGCTCTTTATTTAAGCC | 1147 |

| | | | |
|----|------|---|------|
| QY | 1131 | TAAGGTTTTCCGGATTCAGATCCAAACCTTGCGTTCAAAAATGGAACAACCTTACC | 1130 |
| Db | 1146 | CAGGGTTTTCCGGATTCAGATCCAAACCTTGCGTTCAAAAATGGAACAACCTTACC | 1087 |
| QY | 1191 | GACCGCGCCGGTTATCATCCCTCGGGTGAATGAAATAGCTGATGTAGTCTCAGT | 1250 |
| Db | 1086 | GACCGCGCCGGTTATCATCCCTCGGGTGAATGAAATAGCTGATGTAGTCTCAGT | 1027 |
| QY | 1251 | GAGCCCATATCTTGGCTGATACCTGGCAGATGGAACCTCTTGGCAACCGTTCCCGAC | 1310 |
| Db | 1026 | GAGCCCATATCTTGGCTGATACCTGGCAGATGGAACCTCTTGGCAACCGTTGCGTAT | 967 |
| QY | 1311 | TTCCCTTAGAGGGGAGCGCCACAGAACGATTTCCGTGAATTTAGATTAATCGTATTT | 1370 |
| Db | 966 | TTCCCTTAGAGGTGAGCGCCACAGAACGATTTCCGTGAATTTAGATTAATCGTATTT | 907 |
| QY | 1371 | GTCAATCAGATGCTTTTGCGAAGAAAGAAATAGGATTTGGCAACGACGCACTTGG | 1430 |
| Db | 906 | GTCAATCAGATGCTTTTGCGAAGAAAGAAATAGGATTTGGCAACGACGCACTTGG | 847 |
| QY | 1431 | AATCTGTAATCCGTAAGGCTCCCAAGAACAGCTCTTCTTCAATCTATACATTAAGAC | 1490 |
| Db | 846 | AATCTGTAATCCGTAAGGCTCCCAAGAACAGCTCTTCTTCAATCTATACATTAAGAC | 787 |
| QY | 1491 | GACTCGAATCCACATATCAAAATATCCGAGTGTAGTAAACATTTCCAAAACCGTATGAA | 1550 |
| Db | 786 | GACTCGAATCCACATATCAAAATATCCGAGTGTAGTAAACATTTCCAAAACCGTATGAA | 727 |
| QY | 1551 | TGGAACAACACTTAAATCCGAGATATCCGAAATATTTGATTTGGCAAAAATAGATCTCT | 1610 |
| Db | 726 | TGGAACAACACTTAAATCCGAGATATCCGAAATATTTGATTTGGCAAAAATAGATCTCT | 667 |
| QY | 1611 | GGCATGCGAGAAATCTCAACGAGAGTTCTATAGAGCAGAGCGACCTTATAGCAGAAC | 1670 |
| Db | 666 | GGCATGCGAGAAATCTCAACGAGAGTTCTATAGAGCAGAGCGACCTTATAGCAGAAC | 607 |
| QY | 1671 | AGTAGATCCAGAGAGTTCATGATCAGTGCATTTGCTTGTCCCTATCGAAGACCTTGG | 1730 |
| Db | 606 | AGTAGATCCAGAGAGTTCATGATCAGTGCATTTGCTTGTCCCTATCGAAGAGCTCTGG | 547 |
| QY | 1731 | CACAAATCCGATTCATTAABAAACGGGAGGTAGATGAGTGCAGAACGTTGATATCGA | 1790 |
| Db | 546 | CACAAATCCGATTCATTAABAAACGGGAGGTAGATGAGTGCAGAACGTTGATATCGA | 487 |
| QY | 1791 | CTGAATCCCTGTAATCCGTTTAGAATCCATATATATAATTTTGGATGTAGTTGGAG | 1850 |
| Db | 486 | CTGAATCCCTGTAATCCGTTTAGAATCCATATATATAATTTTGGATGTAGTTGGAG | 427 |
| QY | 1851 | CTTTTTTTGCGGTTCAAAATTTTTTGCAACCCCTTTTGGAAACGAACACACGCTAGG | 1910 |
| Db | 426 | CTTTTTTTGCGGTTCAAAATTTTTTGCAACCCCTTTTGGAAACGAACACACGCTAGG | 367 |
| QY | 1911 | CTGCGAATGCGCATACGTTGAGCAANTCAACGTTCAATTAATGTCTGCGGGCGC | 1970 |
| Db | 366 | CTGCGAATGCGCATACGTTGAGCAANTCAACGTTCAATTAATGTCTGCGGGCGC | 307 |
| QY | 1971 | AACTGCAATCCGATTAATAAACGGCGCCAACAACGGGATTAAGAATTAAGAGAGTTTC | 2030 |
| Db | 306 | AACTGCAATCCGATTAATAAACGGCGCCAACAACGGGATTAAGAATTAAGAGAGTTTC | 247 |
| QY | 2031 | ACTGCAATCGACGATTCGTGATTTGTAATCAGCCCATATCGTTCAATAGCTTCGCCAA | 2090 |
| Db | 246 | ACTGCAATCGACGATTCGTGATTTGTAATCAGCCCATATCGTTCAATAGCTTCGCCAA | 187 |
| QY | 2091 | CCGAACGCACTTTGCAAGTACTCAGCGTAAGTATGCCACCTCGATATATGTGATCTGT | 2150 |
| Db | 186 | CCGAACGCACTTTGCAAGTACTCAGCGTAAGTATGCCACCTCGATATATGTGATCTGT | 127 |
| QY | 2151 | AAAAGCAATGTTCCAGAAACACAGGGGTATCTCTTATAGCTTATAGCAGTTGCTCTCC | 2210 |
| Db | 126 | AAAAGCAATGTTCCAGAAACACAGGGGTATCTCTTATAGCTTATAGCAGTTGCTCTCC | 67 |

Qy 2211 AGCGGTCGCATCTTCACAGCGAGATGAAAGGCGCGCGGCGCTTCTTCTTAAGTTTGGCGTC 2270
Db 66 AGCGGTCGCATCTTCACAGCGAGATGAAAGGCGCGCGGCGCTTCTTCTTAAGTTTGGCGTC 7
Qy 2271 TTTCAT 2276
Db 6 TTTCAT 1

RESULT 14
US-08-354

```

1Sequence 5, Application US/08354240A
2Patent No. 5670356
3GENERAL INFORMATION:
4APPLICANT: Sherf, Bruce A.
5APPLICANT: Wood, Keith V.
6TITLE OF INVENTION: MODIFIED LUCIFERASE
7NUMBER OF SEQUENCES: 20
8CORRESPONDENCE ADDRESS:
9ADDRESSEE: Demit Rose & Stevens, S.C.
10STREET: 8000 Excelbtor Drive, Suite 401
11CITY: Madison
12STATE: WI
13COUNTRY: USA
14ZIP: 53717-1914
15COMPUTER READABLE FORM:
16MEDIUM TYPE: Floppy disk
17COMPUTER: IBM PC compatible
18OPERATING SYSTEM: PC-DOS/MS-DOS
19SOFTWARE: Patent in Release #1.0, Version #1.30
20CURRENT APPLICATION DATA:
21APPLICATION NUMBER: US/08/354,240A
22FILING DATE: 12-DEC-1994
23CLASSIFICATION: 435
24ATTORNEY/AGENT INFORMATION:
25NAME: Sara, Charles S.
26REGISTRATION NUMBER: 30,492
27REFERENCE/DOCKET NUMBER: 34506.029
28TELECOMMUNICATION INFORMATION:
29TELEPHONE: 608-831-2100
30TELEFAX: 608-831-2106
31INFORMATION FOR SEQ ID NO: 5:
32SEQUENCE CHARACTERISTICS:
33LENGTH: 1653 base pairs
34TYPE: nucleic acid
35STRANDEDNESS: single
36TOPOLOGY: linear
37MOLECULE TYPE: cdna
38FRAGMENT TYPE: C-terminal
39ORIGINAL SOURCE:
40ORGANISM: Photinus pyralis
41FEATURE:
42NAME/KEY: CDS
43LOCATION: 1..1650
44US-08-354-240A-5

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| | | | | |
|-----------------------|-----------------|---------------------|-----------|--------------|
| Query Match | 59.3% | Score 1643; | DB 1; | Length 1653; |
| Best Local Similarity | 100.0%; | Pred. No. 5.5e-301; | | |
| Matches 1643; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| QY | 628 | ACGGAGATCTTTCCGCCCTCTTAGGCCCTTATAGAGATCTCTCGATTTTTCTTGCGTCG | 687 |
|----|------|--|------|
| Db | 1652 | ACGGCGATCTTTCCGCCCTCTTAGGCCCTTATAGAGATCTCTCGATTTTTCTTGCGTCG | 1593 |
| QY | 688 | AGTTTTCCGGTAAGACCTTTCGTACTTCGTCCCAAAACAACCTCCGCGCAACTTT | 747 |
| Db | 1592 | AGTTTTCCGGTAAGACCTTTCGTACTTCGTCCCAAAACAACCTCCGCGCAACTTT | 1533 |
| QY | 748 | TTCCGCGTGTACTTACTGACTGGACACGTAATCCACGATCTCTTTTCCGTCATCGTCTTT | 807 |
| Db | 1532 | TTCCGCGTGTACTTACTGACTGGACACGTAATCCACGATCTCTTTTCCGTCATCGTCTTT | 1473 |
| QY | 808 | CCGTGCTTCAAACAACACGCGCGCGGAAATTCAACGCGTCATCGTCGGAAGACT | 867 |

| | | | | |
|----|------|--|----------------------|------|
| Db | 1472 | CCGGTCTCAAAACAAACACGCGCGGGAAGTTTCA | CGCGGTCATCTCGGAAACCT | 1413 |
| OY | 868 | GCACACCTGGTGCAGAGATGTTGGGGGTGGAGACAAGATGATGTTCCAAATTCACCGGGA | | 927 |
| Db | 1412 | GCACACCTGGTGCAGAGATGTTGGGGGTGGAGACAAGATGATGTTCCAAATTCACCGGGA | | 1355 |
| OY | 928 | GCCACCTGATAGCTTTGTACTTAATCAAGACTTCAAGCGGTCAACGATGAAGATGT | | 987 |
| Db | 1352 | GCCACCTGATAGCTTTGTACTTAATCAAGACTTCAAGCGGTCAACGATGAAGATGT | | 1293 |
| OY | 988 | TGCGTTCGTCCCGATAGCTATGTCCTCAAAATGTAAGCCATCCATCCTTGTCAATCAAG | | 1047 |
| Db | 1292 | TGCGTTCGTCCCGATAGCTATGTCCTCAAAATGTAAGCCATCCATCCTTGTCAATCAAG | | 1233 |
| OY | 1048 | GCGTGTGTCGCTTCGGAATGTTTATCAATAACGGACATATCATAGACCTCTCACAC | | 1107 |
| Db | 1232 | GCGTGTGTCGCTTCGGAATGTTTATCAATAACGGACATATCATAGACCTCTCACAC | | 1173 |
| OY | 1108 | AGTTGCGCTCTTGATTTAACGCCACGCGTTTCCCGGTATCCAGATCCAACTTCGCT | | 1167 |
| Db | 1172 | AGTTGCGCTCTTGATTTAACGCCACGCGTTTCCCGGTATCCAGATCCAACTTCGCT | | 1113 |
| OY | 1168 | TCAAAAAATGGAACAACCTTACCGACCGCGCCGGTTTATCAATCCCTCGGGTGTATC | | 1227 |
| Db | 1112 | TCAAAAAATGGAACAACCTTACCGACCGCGCCGGTTTATCAATCCCTCGGGTGTATC | | 1053 |
| OY | 1228 | AGAAATAGCTATGTAGTCTCAGTAGGCCATATCCTTGCTGATACCTGGGAGATGGAAC | | 1287 |
| Db | 1052 | AGAAATAGCTATGTAGTCTCAGTAGGCCATATCCTTGCTGATACCTGGGAGATGGAAC | | 993 |
| OY | 1288 | CTCTTGGCAACCGCTTCCCGCACTTCTTACAGAGGGAGCGCCACGAAACATTTGCG | | 1347 |
| Db | 992 | CTCTTGGCAACCGCTTCCCGCACTTCTTACAGAGGGAGCGCCACGAAACATTTGCG | | 933 |
| OY | 1348 | TGTAATTAAGTAATGATGTTTGTCAATCAGAGTCTTTTGGGGAAGAGAGATATAG | | 1407 |
| Db | 932 | TGTAATTAAGTAATGATGTTTGTCAATCAGAGTCTTTTGGGGAAGAGAGATATAG | | 873 |
| OY | 1408 | GTTGGACACACACGCGCACTTGAATCTGTAATCTCGAAGGCTCTCAGAAACAGCTCT | | 1467 |
| Db | 872 | GTTGGACACACACGCGCACTTGAATCTGTAATCTCGAAGGCTCTCAGAAACAGCTCT | | 813 |
| OY | 1468 | TCTTCAATCTATACATTTAAGACGACTGAAATCCACATATCAAAATATCCGAGTGTAGTA | | 1527 |
| Db | 812 | TCTTCAATCTATACATTTAAGACGACTGAAATCCACATATCAAAATATCCGAGTGTAGTA | | 753 |
| OY | 1528 | AACATTCCAAAACCGTATGGAATGGAACAACAACCTTAAATCCGATATCCGGAATGATT | | 1587 |
| Db | 752 | AACATTCCAAAACCGTATGGAATGGAACAACAACCTTAAATCCGATATCCGGAATGATT | | 693 |
| OY | 1588 | TGATTTGCCAAAAATAGGATCTCTGCGATTCGAGAAATCTCACGCGAGGAGTTCTATGAGGC | | 1647 |
| Db | 692 | TGATTTGCCAAAAATAGGATCTCTGCGATTCGAGAAATCTCACGCGAGGAGTTCTATGAGGC | | 633 |
| OY | 1648 | AGACGCAACCTTTAGGCGAGCCAGTAGATCCAGAGAGTTCAATCAATGCAATTTGTC | | 1707 |
| Db | 632 | AGACGCAACCTTTAGGCGAGCCAGTAGATCCAGAGAGTTCAATCAATGCAATTTGTC | | 573 |
| OY | 1708 | TTGTTCCTATCGAAGACTCTGCGCAAAATCGTATTCAATTAACCGGAGGTAGATGA | | 1767 |
| Db | 572 | TTGTTCCTATCGAAGACTCTGCGCAAAATCGTATTCAATTAACCGGAGGTAGATGA | | 513 |
| OY | 1768 | GATGTGACGAACGTTGATCATCGACTGAAATCCCTGATATCCCGTTTAAAGATCCATGATA | | 1827 |
| Db | 512 | GATGTGACGAACGTTGATCATCGACTGAAATCCCTGATATCCCGTTTAAAGATCCATGATA | | 453 |
| OY | 1828 | ATAATTTTTTGATGATTTGGAGAGCTTTTTTTTGACGTTCAAAATTTTTTGCAACCCCTTT | | 1887 |
| Db | 452 | ATAATTTTTTGATGATTTGGAGAGCTTTTTTTTGACGTTCAAAATTTTTTTGCAACCCCTTT | | 393 |
| OY | 1888 | TTGGAAACGAACACGATAGCGTTCGAAATGCCATCTGTTAGCAATTCACGTTCA | | 1947 |

Db 392 TTGAAGACGACACCGGTAGCTGCGAATGCCATCTGTGAGCAATTCAAGTTCA 333
 Qy 1948 TTATAATGCTGTTGGCGGCGCACTGAACTCCGATAATTAACCGCCCAACCGCGC 2007
 Db 332 TTATAATGCTGTTGGCGGCGCACTGAACTCCGATAATTAACCGCCCAACCGCGC 273
 Qy 2008 ATAAAGAAATTGAAGAGATTTCACATGACGATCGATCTGTGATTTGATTCAGCCCA 2067
 Db 212 ATAAAGAAATTGAAGAGATTTCACATGACGATCGATCTGTGATTTGATTCAGCCCA 213
 Qy 2068 TATGCTTATAGCTTCTGCAACCGAAGCAATTGGAAGTACTCAGCGTAAGTATG 2127
 Db 212 TATGCTTATAGCTTCTGCAACCGAAGCAATTGGAAGTACTCAGCGTAAGTATG 153
 Qy 2128 TCCACCTGATATGTCATCTGTAAAGAAATTGTCAGGAACCAAGGCGTATCTTTC 2187
 Db 152 TCCACCTGATATGTCATCTGTAAAGAAATTGTCAGGAACCAAGGCGTATCTTTC 93
 Qy 2188 ATAGCTTATGAGTTGCTCTCAGCGGTTCCATCTTCCAGCGGATAGAAATGCGCGG 2247
 Db 92 ATAGCTTATGAGTTGCTCTCAGCGGTTCCATCTTCCAGCGGATAGAAATGCGCGG 33
 Qy 2248 CCTTCTTATGTTTTTGGCGTC 2270
 Db 32 CCTTCTTATGTTTTTGGCGTC 10

RESULT 15
 US-09-602-628-1/c
 ; Sequence 1, Application US/09602628
 ; Patent No. 6495355
 ; GENERAL INFORMATION:
 ; APPLICANT: Eames, Brian
 ; APPLICANT: Conlag, Christopher
 ; TITLE OF INVENTION: Red-Shifted Luciferase
 ; FILE REFERENCE: SUN-127
 ; CURRENT APPLICATION NUMBER: US/09/602,628
 ; CURRENT FILING DATE: 2000-06-21
 ; PRIOR APPLICATION NUMBER: 60/140,598
 ; PRIOR FILING DATE: 1999-06-22
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1686
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1650)
 US-09-602-628-1

Query Match 59.3%; Score 1642.8; DB 4; Length 1686;
 Best Local Similarity 98.4%; Pred. No. 6e-301;
 Matches 1659; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
 Qy 591 TGGCTTAAGAGCGCGGATGTTTACCCCAACCTTTAAAGCGGATTTTCCGCTTCTT 650
 Db 1686 TGGCTTAAGAGCGCGGATGTTTACCCCAACCTTTAAAGCGGATTTTCCGCTTCTT 1627
 Qy 651 GGCCTTATGAGGATCTCTGATTTTCTGCGTGAAGTTTCCGGTAAGACCTTTCGG 710
 Db 1626 GGCCTTATGAGGATCTCTGATTTTCTGCGTGAAGTTTCCGGTAAGACCTTTCGG 1567
 Qy 711 TACTTCGTCCACAAACAACTCTCCGCGCACTTTTCCGCGTGTACTTGAAGTGC 770
 Db 1566 TACTTCGTCCACAAACAACTCTCCGCGCACTTTTCCGCGTGTACTTGAAGTGC 1507
 Qy 771 GACGTAATCCAGATCTCTTTTCCGTCACTCTTCCGTGCTCCAAACCAACGCGC 830
 Db 1506 GACGTAATCCAGATCTCTTTTCCGTCACTCTTCCGTGCTCCAAACCAACGCGC 1447
 Qy 831 GCGGGAAGTTACCGCGCTCAGTCGTGGGAAGACCTGGGACACCTGCGTCAAGATGTT 890

Db 1446 GCGGGAAGTTACCGCGCTCAGTCGTGGGAAGACCTCGACACCTGCGTCAAGATGTT 1387
 Qy 891 GGGGTGTTGAGCAAGATGATTTCCAAATTCACCGGAGCAACCTGATGCTTTGACTT 950
 Db 1386 GGGGTGTTGAGCAAGATGATTTCCAAATTCAGTGGAGCACCTGATGCTTTGACTT 1327
 Qy 951 ATCAGAGACTTCAGCGGTCACAGATGAGAAAGTGTCTGCTTGTCCAGTAAGTAT 1010
 Db 1326 ATCAGAGACTTCAGCGGTCACAGATGAGAAAGTGTCTGCTTGTCCAGTAAGTAT 1267
 Qy 1011 GTCTCAGAAATGATCCATCCATCTTGTCAATCAAGGCGTTGCTTCCGAATGTT 1070
 Db 1266 GTCTCAGAAATGATCCATCCATCTTGTCAATCAAGGCGTTGCTTCCGAATGTT 1207
 Qy 1071 TACATTAACCGGACATATCATAGACCTCTCAACAAGTTCGCTCTTGAATTAACGC 1130
 Db 1206 TACATTAACCGGACATATCATAGACCTCTCAACAAGTTCGCTCTTGAATTAACGC 1147
 Qy 1131 CAGGTTTTCCCGGTATCCAGATCCAGTCCAAACCTTCAAAAATGGAACAATTAC 1190
 Db 1146 CAGGTTTTCCCGGTATCCAGATCCAGTCCAAACCTTCAAAAATGGAACAATTAC 1087
 Qy 1191 GACCGCGCCGCTTATCATCCCTCCGCTGTAATCAGAAATGCTGATGCTCACT 1250
 Db 1086 GACCGCGCCGCTTATCATCCCTCCGCTGTAATCAGAAATGCTGATGCTCACT 1027
 Qy 1251 GAGCCCATATCTTCTGCTGATCTGCGAGATGGAACCTCTTGGCAACCGCTCCCGAC 1310
 Db 1026 GAGCCCATATCTTCTGCTGATCTGCGAGATGGAACCTCTTGGCAACCGCTCCCGAC 967
 Qy 1311 TTCCTTAAGAGAGGAGCGCCACAGAAAGCAATTCGTGTAATTAATTAATTCGATTT 1370
 Db 966 TTCCTTAAGAGAGGAGCGCCACAGAAAGCAATTCGTGTAATTAATTAATTCGATTT 907
 Qy 1371 GTCAATCAAGATGCTTTTGGCGAAGAGAGATAGGTTGGCACAGAGCGCACTTGG 1430
 Db 906 GTCAATCAAGATGCTTTTGGCGAAGAGAGATAGGTTGGCACAGAGCGCACTTGG 847
 Qy 1431 AATCTTGAATCTTGAAGGCTCTCTGAAGAAACGCTCTTCTTAATCTTAATTAAGC 1490
 Db 846 AATCTTGAATCTTGAAGGCTCTCTGAAGAAACGCTCTTCTTAATCTTAATTAAGC 787
 Qy 1491 GACTGAATCCAGATCAATCAAAATATCCAGATGATGTAAGATTCGCAAAACGATGGA 1550
 Db 786 GACTGAATCCAGATCAATCAAAATATCCAGATGATGTAAGATTCGCAAAACGATGGA 727
 Qy 1551 TGGAAACAACCTTAATAATCGCAGATCCGGAATGATTTGATTCGCAAAATAGATCT 1610
 Db 726 TGGAAACAACCTTAATAATCGCAGATCCGGAATGATTTGATTCGCAAAATAGATCT 667
 Qy 1611 GGCATGCGAAGATCTCAGCGAGGAGTCTATAGGCGAGAGGACCTTTAGCGAGAC 1670
 Db 666 GGCATGCGAAGATCTCAGCGAGGAGTCTATAGGCGAGAGGACCTTTAGCGAGAC 607
 Qy 1671 AGTAATCCAGAGGATCATGATCAGTGCATTTGCTTGTCCATGGAAGACTCTGG 1730
 Db 606 AGTAATCCAGAGGATCATGATCAGTGCATTTGCTTGTCCATGGAAGACTCTGG 547
 Qy 1731 CACAAATCGTATTAATAAACCGGAGGTAGATGAGATGGAAGAGCTGTACATGCA 1790
 Db 546 CACAAATCGTATTAATAAACCGGAGGTAGATGAGATGGAAGAGCTGTACATGCA 487
 Qy 1791 CTGAATCCCTGATATCCGTTTGAATCCATGATTAATTTTGGATGATTTGGAG 1850
 Db 486 CTGAATCCCTGATATCCGTTTGAATCCATGATTAATTTTGGATGATTTGGAG 427
 Qy 1851 CTTTTTTCAGCTCAAAATTTTTCGACCCCTTTTGGAAAGAGACCAACGCTGAG 1910
 Db 426 CTTTTTTCAGCTCAAAATTTTTCGACCCCTTTTGGAAAGAGACCAACGCTGAG 367
 Qy 1911 CTGCAAAATGCCCATACTGTTGAGCAATTCAGCTTCATTAATGTCGTTGCGCGCGC 1970

| | | | |
|----|------|---|------|
| Db | 366 | CTGGAAATGCCATACCTGTTGACCAATTCAGTTCAATTATTAATGTCGTCGGGCGC | 307 |
| Qy | 1971 | AACTGAACCTCCGATAAATAACGGCCCAACACGGGCATAAAGAAATTGAAGAGTTTC | 2030 |
| Db | 306 | AACAGCACTCCGATAAATAACGGCCCAACACGGGCATAAAGAAATTGAAGAGTTTC | 247 |
| Qy | 2031 | ACTGCATACGACGATTCGTGATTTGTATTCAGCCCATATGTTTCATAGCTTCGCCAA | 2090 |
| Db | 246 | ACTGCATACGACGATTCGTGATTTGTATTCAGCCCATATGTTTCATAGCTTCGCCAA | 187 |
| Qy | 2091 | CCGAACGGACATTTCCGAAGTACTCAGCGTAAGTATGTCACCTCGATATGTGCATCTGT | 2150 |
| Db | 186 | CCGAACGGACATTTCCGAAGTACTCAGCGTAAGTATGTCACCTCGATATGTGCATCTGT | 127 |
| Qy | 2151 | AAAAGCAATTGTTCCAGGAAACAGGGGATCTCTCATAGCCCTTATGCAAGTTGCTCC | 2210 |
| Db | 126 | AAAAGCAATTGTTCCAGGAAACAGGGGATCTCTCATAGCCCTTATGCAAGTTGCTCC | 67 |
| Qy | 2211 | AGCGTTCCATCTTCCAGCGGATGAAATGGCGCCGACCTTTCCTTATGTTTGGCGTC | 2270 |
| Db | 66 | AGCGTTCCATCTTCCAGCGGATGAAATGGCGCCGACCTTTCCTTATGTTTGGCGTC | 7 |
| Qy | 2271 | TTCCAT 2276 | |
| Db | 6 | TTCCAT 1 | |

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 Job time : 460 secs